

FIGURE 1

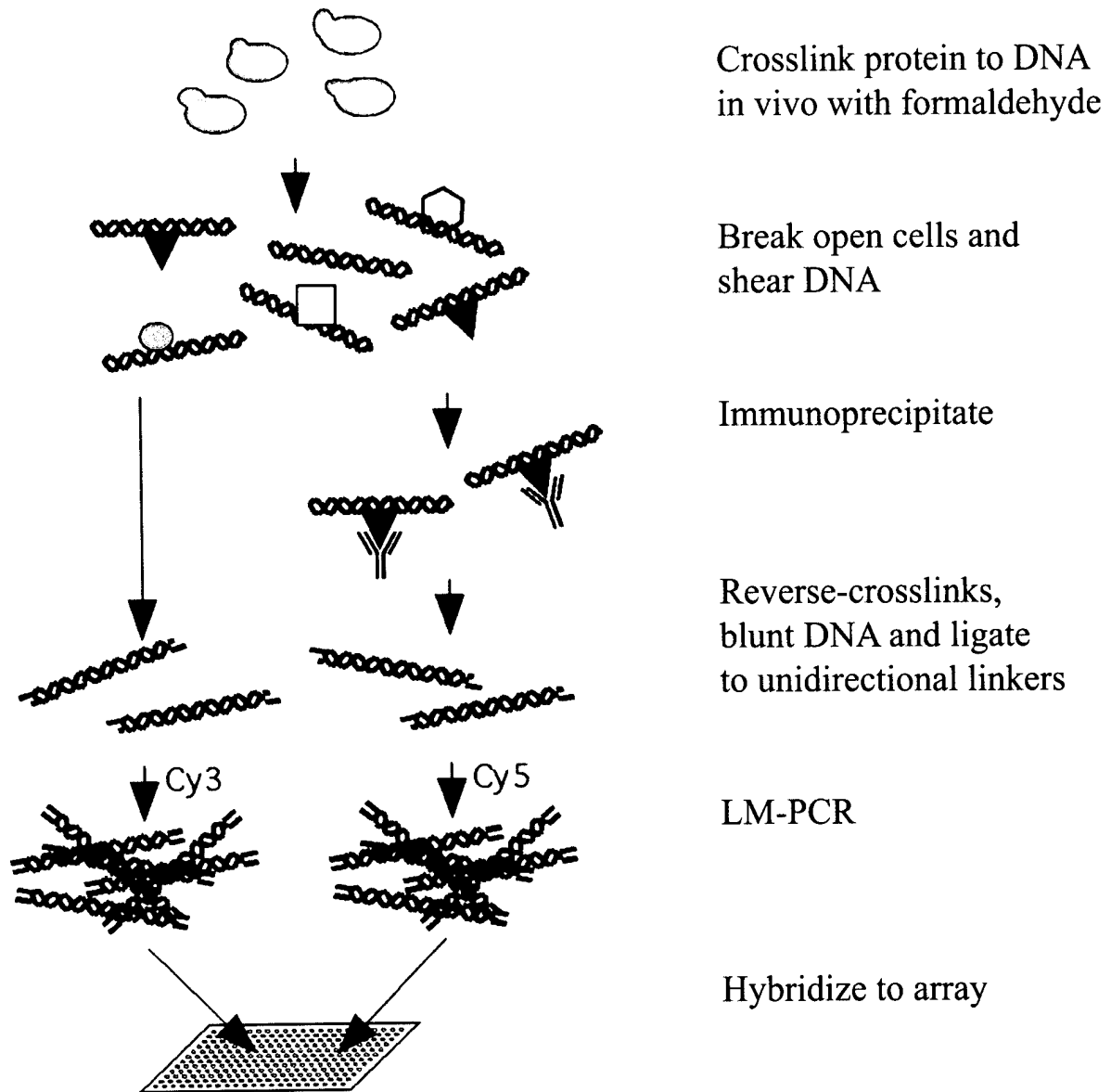


FIGURE 1



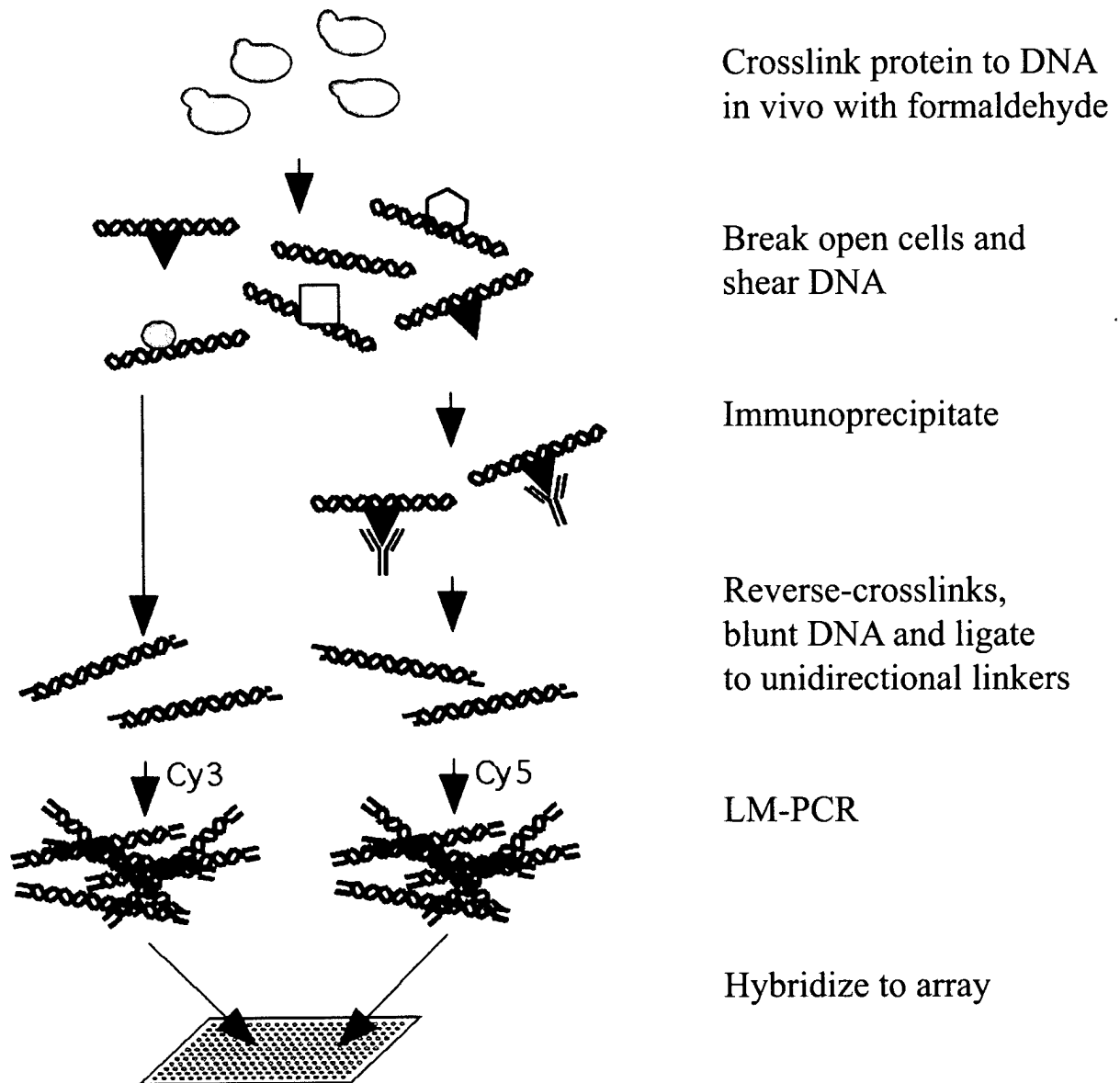


FIGURE 1

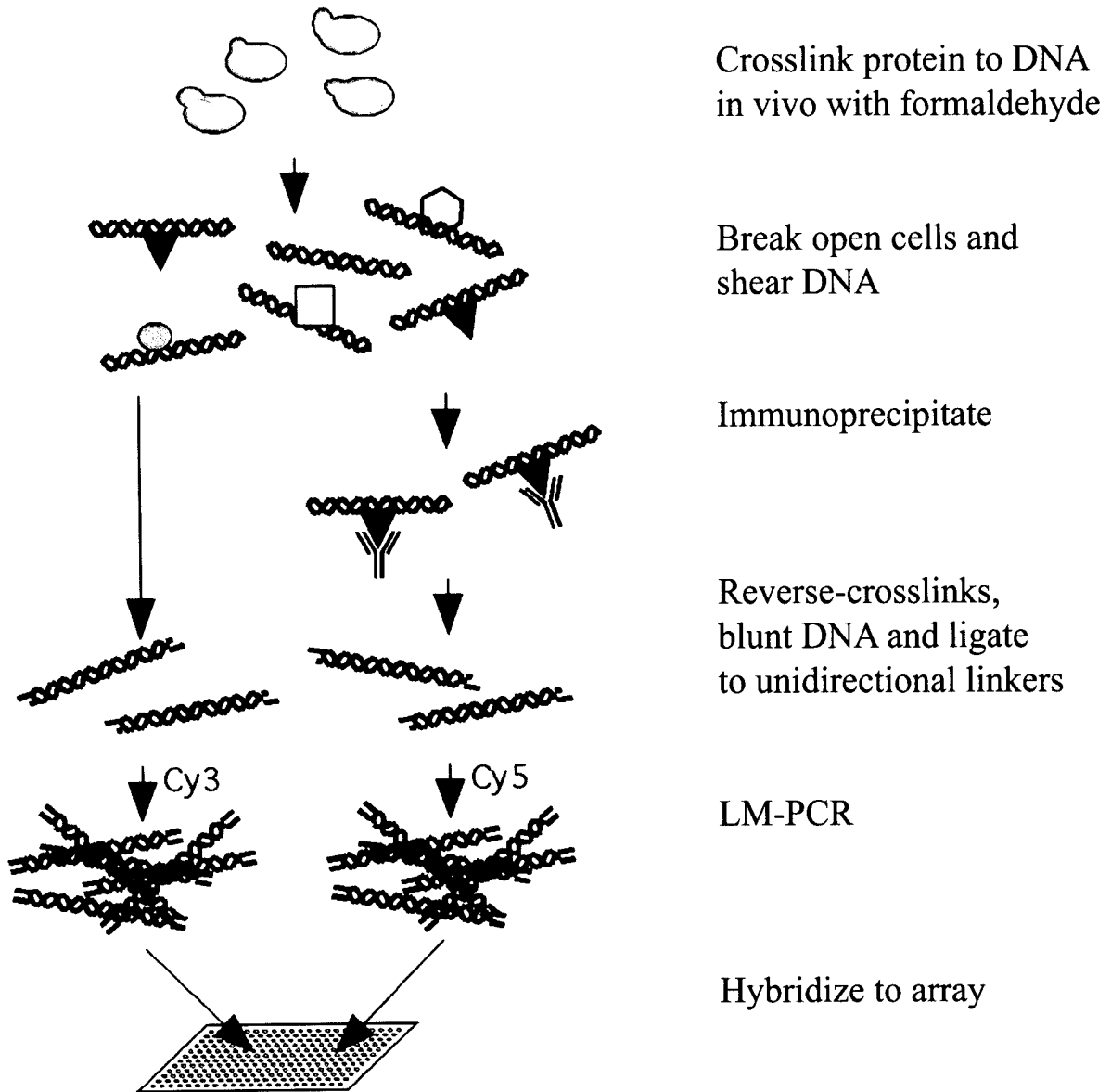


FIGURE 1

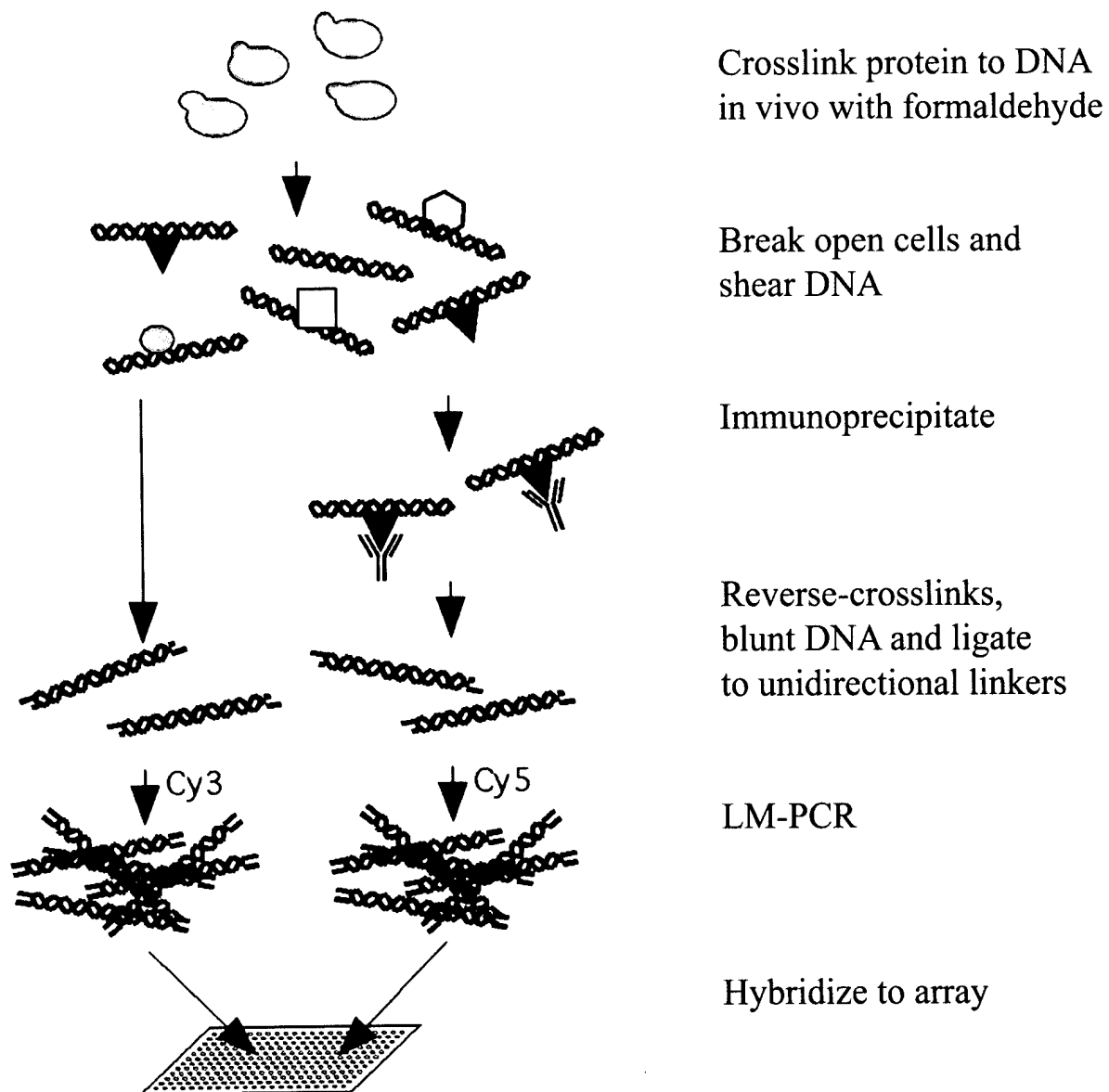


FIGURE 1

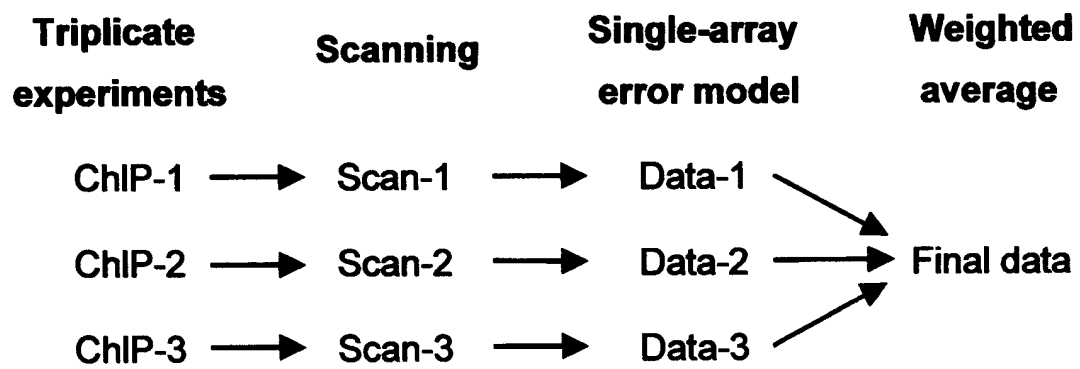


FIGURE 2

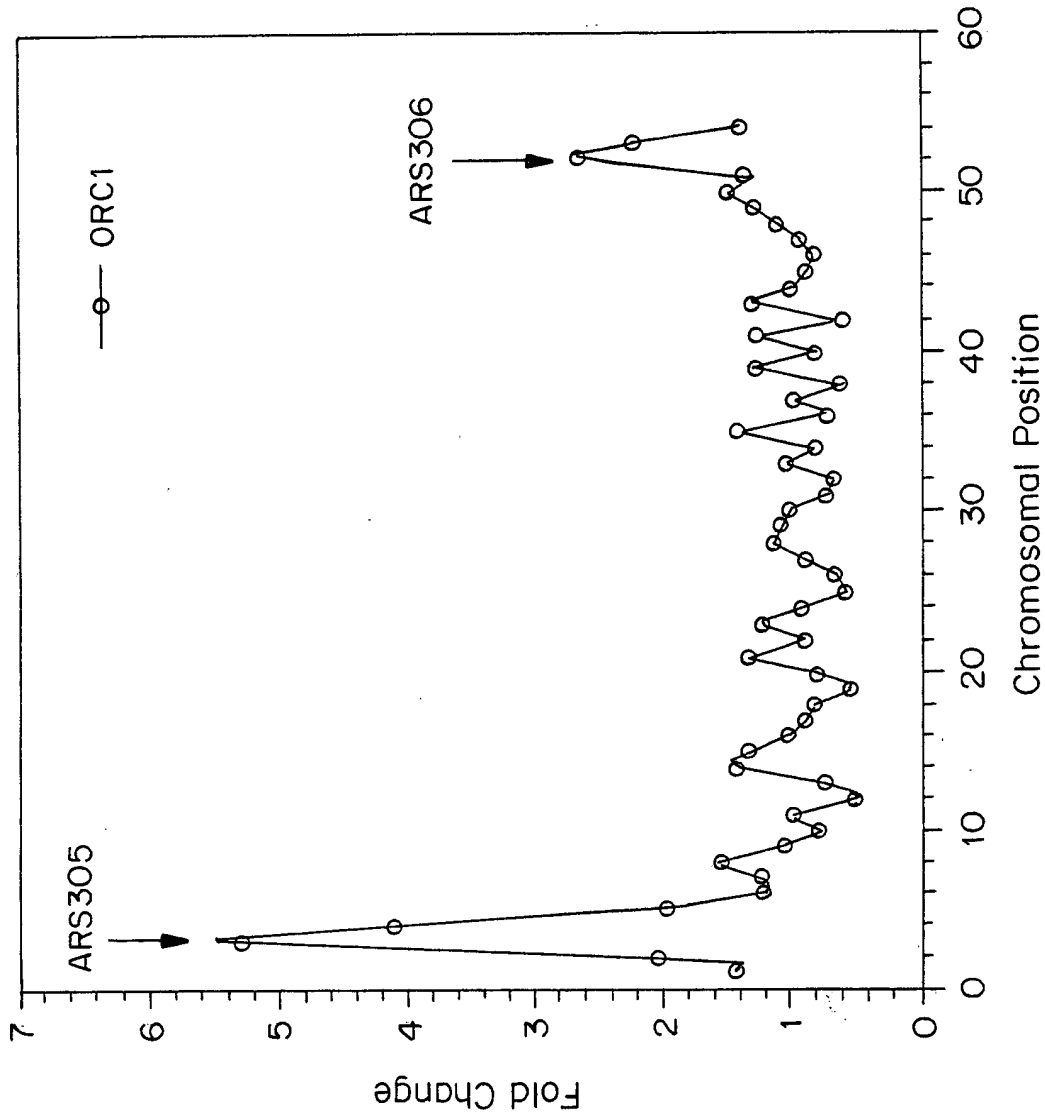


FIG. 3

Interests:
 RNA Polymerase II
 SRB/Mediator Complex
 General Transcription Factors
 SWI/SNF Complex
 SAGA
 ORC complex
 DNA Polymerase

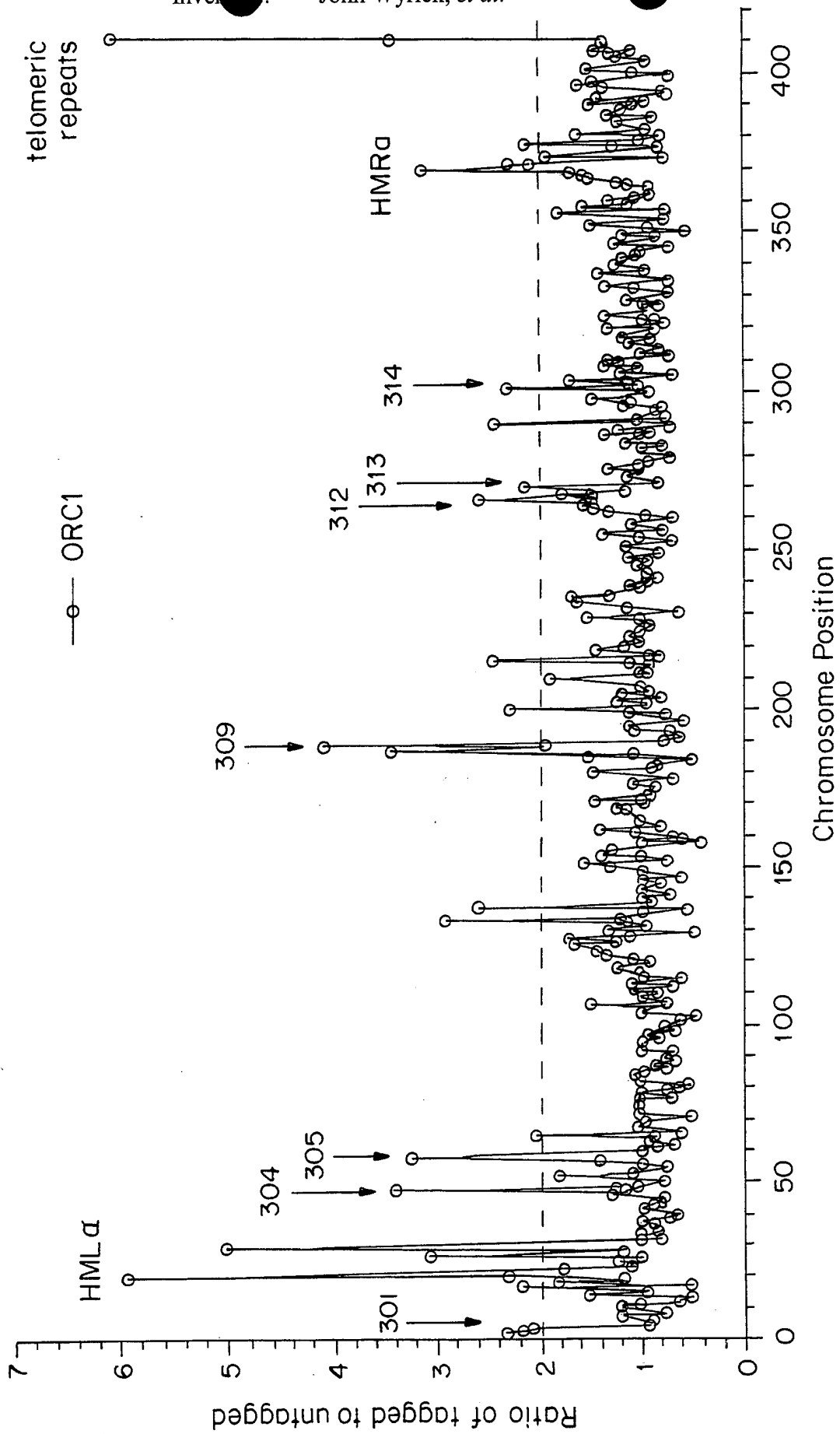


FIG. 4

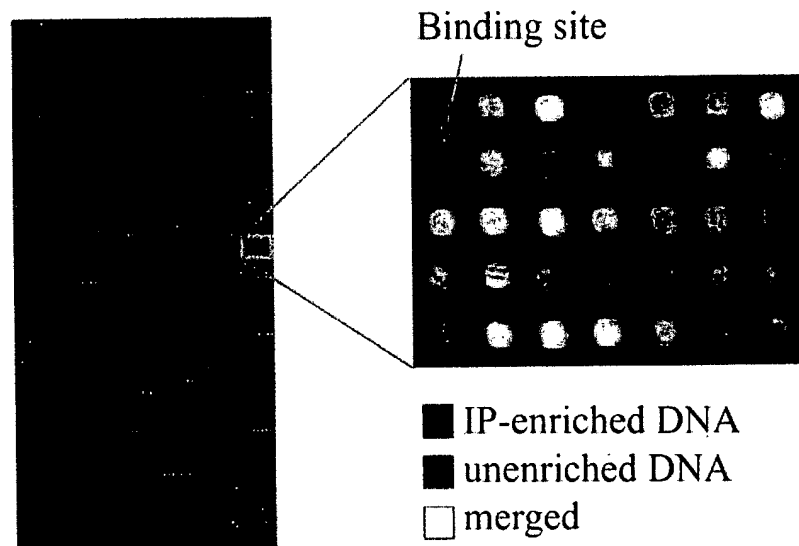


FIGURE 5A

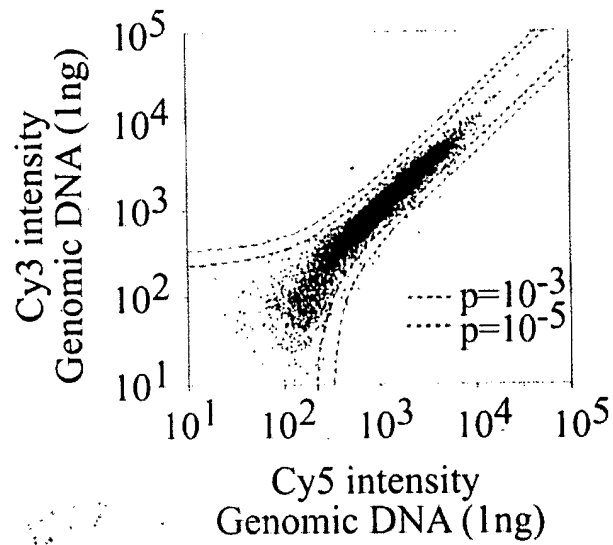


FIGURE 5B

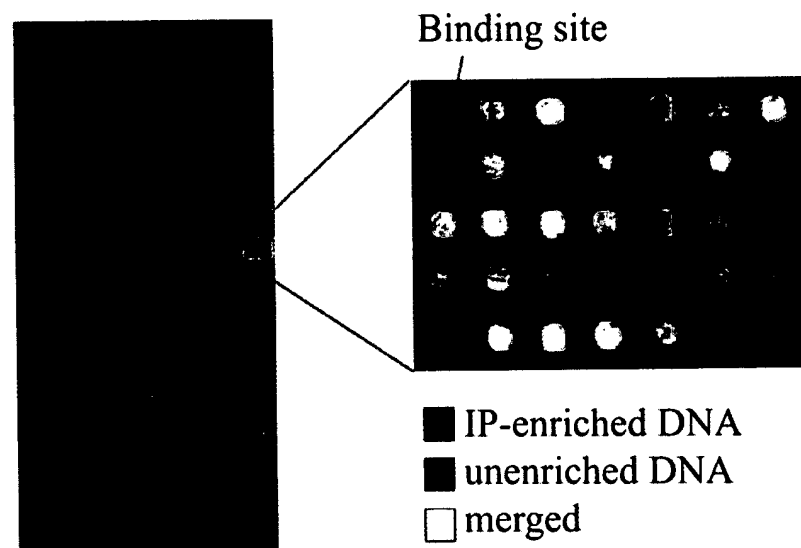


FIGURE 5A

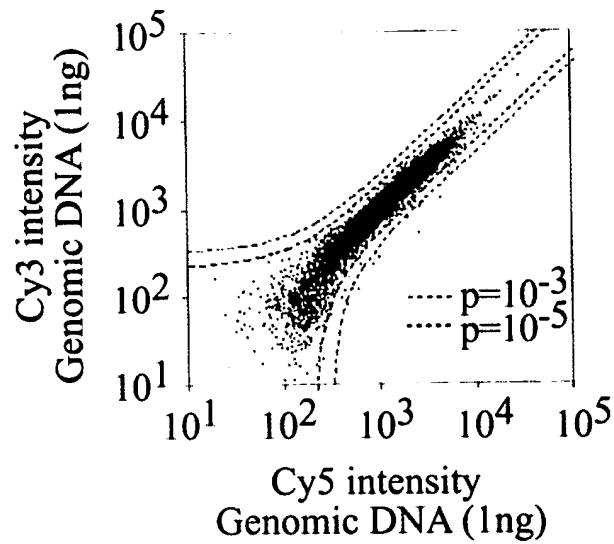


FIGURE 5B

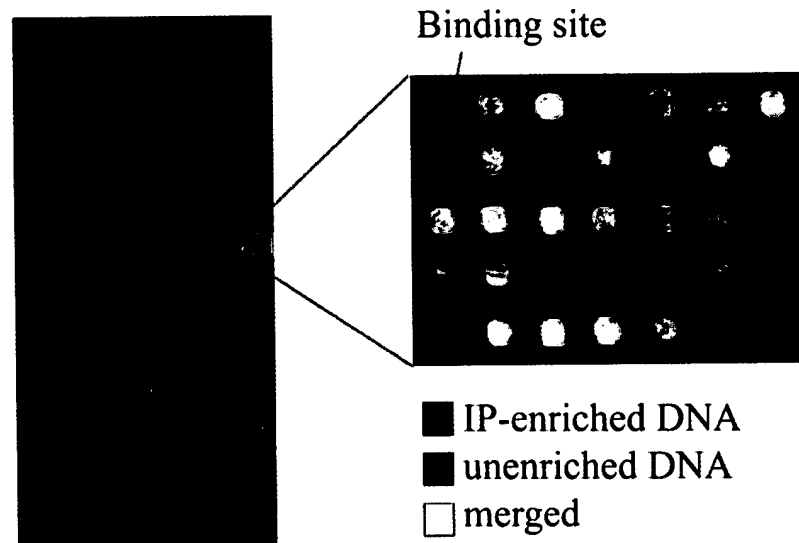


FIGURE 5A

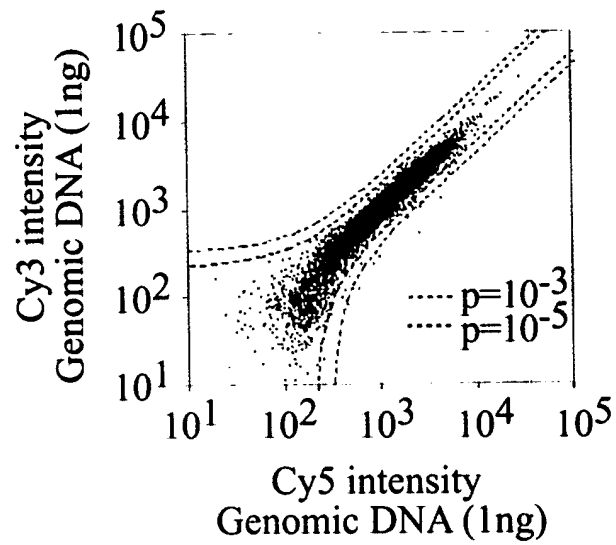


FIGURE 5B

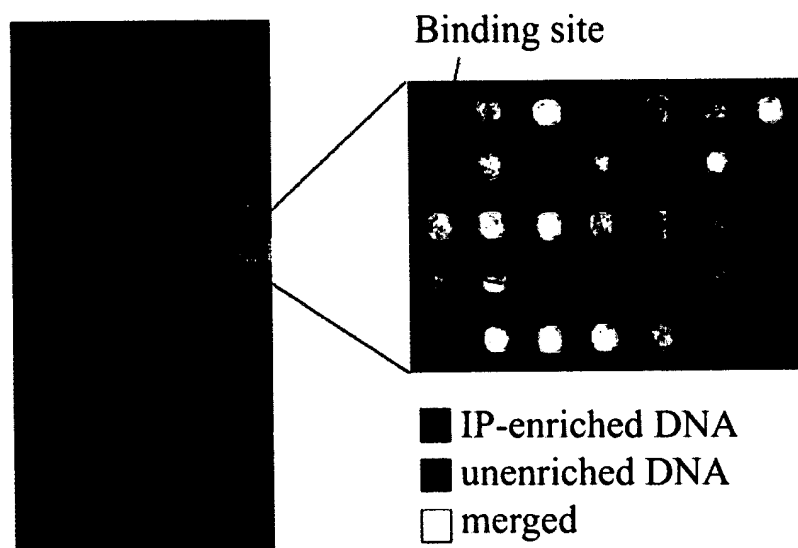


FIGURE 5A

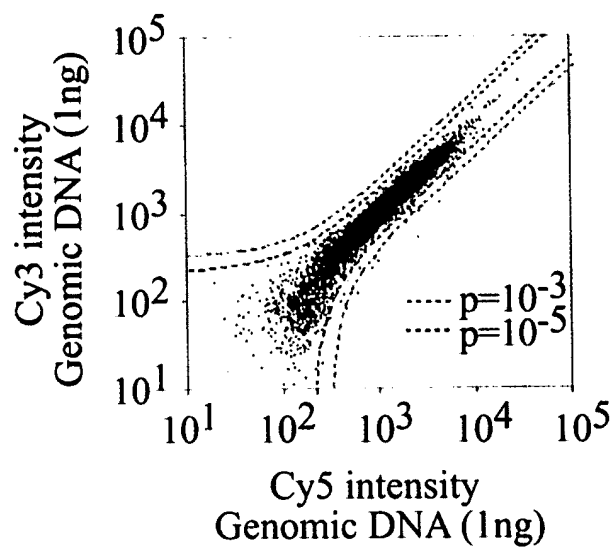


FIGURE 5B

Glucose	Galactose	Expression (Gal/Glu)	Name	Binding		Expression	
				Glucose		Galactose	
				Ratio	p-value	Ratio	p-value
			GAL2	2.8	2.5X10 ⁻⁰²	9.5	1.5X10 ⁻¹⁰
			GAL3	1.4	5.4X10 ⁻⁰¹	8.2	3.5X10 ⁻¹⁰
			GAL7	0.4	2.0X10 ⁺⁰⁰	8.2	6.4X10 ⁻¹⁰
			GAL1	1.3	6.0X10 ⁻⁰¹	7.8	1.5X10 ⁻⁰⁹
			GAL10	1.3	6.0X10 ⁻⁰¹	7.8	1.5X10 ⁻⁰⁹
			FUR4	0.3	2.0X10 ⁺⁰⁰	4.6	4.3X10 ⁻⁰⁸
			GCY1	0.9	1.2X10 ⁺⁰⁰	4.3	1.3X10 ⁻⁰⁷
			MTH1	0.9	1.2X10 ⁺⁰⁰	4.0	2.4X10 ⁻⁰⁷
			GAL80	0.5	1.9X10 ⁺⁰⁰	3.7	7.0X10 ⁻⁰⁷
			PCL10	0.6	1.8X10 ⁺⁰⁰	3.0	8.8X10 ⁻⁰⁶
			YBR022W	3.7	1.7X10 ⁻⁰²	10.4	1.2X10 ⁻¹⁰
			YDR008C	1.4	5.5X10 ⁻⁰¹	8.2	3.5X10 ⁻¹⁰
			GIS3	2.7	2.9X10 ⁻⁰²	8.0	4.8X10 ⁻¹⁰
			TLC1	0.6	1.9X10 ⁺⁰⁰	4.2	1.2X10 ⁻⁰⁷
			PDX3	0.6	1.9X10 ⁺⁰⁰	4.2	1.2X10 ⁻⁰⁷
			RIO1	0.9	1.2X10 ⁺⁰⁰	4.3	1.3X10 ⁻⁰⁷
			YJR044C	2.3	6.6X10 ⁻⁰²	4.0	3.4X10 ⁻⁰⁷
			SNQ2	0.9	1.1X10 ⁺⁰⁰	3.5	1.1X10 ⁻⁰⁶
			YDR010C	0.9	1.1X10 ⁺⁰⁰	3.5	1.1X10 ⁻⁰⁶
			APC9	1.9	1.9X10 ⁻⁰¹	3.8	2.0X10 ⁻⁰⁶
			CSG2	0.5	1.9X10 ⁺⁰⁰	3.3	2.4X10 ⁻⁰⁶
			RPL4B	0.9	1.3X10 ⁺⁰⁰	3.3	2.8X10 ⁻⁰⁶
			YGL132W	0.6	1.8X10 ⁺⁰⁰	3.0	9.1X10 ⁻⁰⁶
			CHA4	1.5	4.1X10 ⁻⁰¹	3.1	9.8X10 ⁻⁰⁶

<1:1 >3/1 >5/1 <1/5 1/1 >5/1

FIGURE 6A

Glucose	Galactose	Binding		Name	Expression (Gal/Glu)	Binding		Ratio	Gal/Glu	Description
		Glucose				Galactose				
		Ratio	p-value			Ratio	p-value			
		2.8	2.5X10-02	9.5	1.5X10-10	188.6				Galactose permease
		1.4	5.4X10-01	8.2	3.5X10-10	18.2				Regulatory protein required for rapid induction of galactose pathway
		0.4	2.0X10+00	8.2	6.4X10-10	170.1				UDP-glucose-hexose-1-phosphate uridylyltransferase
		1.3	6.0X10-01	7.8	1.5X10-09	271.3				Galactokinase, first step in galactose metabolism
		1.3	6.0X10-01	7.8	1.5X10-09	118.8				UDP-glucose 4-epimerase
		0.3	2.0X10+00	4.6	4.3X10-08	4.6				Uracil permease (adjacent to GAL1)
		0.9	1.2X10+00	4.3	1.3X10-07	93.1				Galactose-induced oxidoreductase
		0.9	1.2X10+00	4.0	2.4X10-07	21.6				Repressor of hexose transport genes
		0.5	1.9X10+00	3.7	7.0X10-07	4.0				Negative regulator for expression of galactose-induced genes
		0.6	1.8X10+00	3.0	8.8X10-06	2.6				Cyclin that associates with Pho85p, involved in glycogen accumulation
		3.7	1.7X10-02	10.4	1.2X10-10	1.5				Unknown function (adjacent to GAL1)
		1.4	5.5X10-01	8.2	3.5X10-10	1.5				Unknown function (share intergenic region with GAL3)
		2.7	2.9X10-02	8.0	4.8X10-10	1.0				Multicopy suppressor of the Gal(-) phenotype of snf1 mig1 strb8/10/11 cells
		0.6	1.9X10+00	4.2	1.2X10-07	1.0				RNA subunit of telomerase
		0.6	1.9X10+00	4.2	1.2X10-07	1.6				Pyridoxine phosphate oxidase
		0.9	1.2X10+00	4.3	1.3X10-07	1.4				Unknown function (share intergenic region with GCY1)
		2.3	6.6X10-02	4.0	3.4X10-07	1.7				Unknown function
		0.9	1.1X10+00	3.5	1.1X10-06	0.6				Drug-efflux pump involved in resistance to multiple drugs (adjacent to GAL3)
		0.9	1.1X10+00	3.5	1.1X10-06	1.0				Unknown function (adjacent to GAL3)
		1.9	1.9X10-01	3.8	2.0X10-06	1.2				Component of the anaphase-promoting complex (APC)
		0.5	1.9X10+00	3.3	2.4X10-06	1.3				Required for synthesis of the mannosylated sphingolipids
		0.9	1.3X10+00	3.3	2.8X10-06	0.8				Ribosomal protein L4, Gene (adjacent to GAL3)
		0.6	1.8X10+00	3.0	9.1X10-06	1.0				Unknown function, (adjacent to PCL10)
		1.5	4.1X10-01	3.1	9.8X10-06	1.0				Zinc-finger protein required for transcriptional activation of CHA1
<div><div><1:1</div><div>>3/1</div><div>>5/1</div><div><1/5</div><div>1/1</div><div>>5/1</div></div>										

FIGURE 6A

Binding Glucose	Expression (Gal/Glu)	Name	Binding		Expression
			Glucose Ratio p-value	Galactose Ratio p-value	Ratio Gal/Glu Description
		GAL2	2.8 2.5X10-02	9.5 1.5X10-10	188.6 Galactose permease
		GAL3	1.4 5.4X10-01	8.2 3.5X10-10	18.2 Regulatory protein required for rapid induction of galactose pathway
		GAL7	0.4 2.0X10+00	8.2 6.4X10-10	170.1 UDP-glucose-hexose-1-phosphate uridylyltransferase
		GAL1	1.3 6.0X10-01	7.8 1.5X10-09	271.3 Galactokinase, first step in galactose metabolism
		GAL10	1.3 6.0X10-01	7.8 1.5X10-09	118.8 UDP-glucose 4-epimerase
		FUR4	0.3 2.0X10+00	4.6 4.3X10-08	4.6 Uracil permease (adjacent to GAL1)
		GCY1	0.9 1.2X10+00	4.3 1.3X10-07	93.1 Galactose-induced oxidoreductase
		MTH1	0.9 1.2X10+00	4.0 2.4X10-07	21.6 Repressor of hexose transport genes
		GAL80	0.5 1.9X10+00	3.7 7.0X10-07	4.0 Negative regulator for expression of galactose-induced genes
		PCL10	0.6 1.8X10+00	3.0 8.8X10-06	2.6 Cyclin that associates with Pho85p, involved in glycogen accumulation
		YBR022W	3.7 1.7X10-02	10.4 1.2X10-10	1.5 Unknown function (adjacent to GAL1)
		YDR008C	1.4 5.5X10-01	8.2 3.5X10-10	1.5 Unknown function (share intergenic region with GAL3)
		GIS3	2.7 2.9X10-02	8.0 4.8X10-10	1.0 Multicopy suppressor of the Gal(-) phenotype of snf1 mig1 srb8/10/11 cells
		TLC1	0.6 1.9X10+00	4.2 1.2X10-07	1.0 RNA subunit of telomerase
		PDX3	0.6 1.9X10+00	4.2 1.2X10-07	1.6 Pyridoxine phosphate oxidase
		RIO1	0.9 1.2X10+00	4.3 1.3X10-07	1.4 Unknown function (share intergenic region with GCY1)
		YJR044C	2.3 6.6X10-02	4.0 3.4X10-07	1.7 Unknown function
		SNQ2	0.9 1.1X10+00	3.5 1.1X10-06	0.6 Drug-efflux pump involved in resistance to multiple drugs (adjacent to GAL3)
		YDR010C	0.9 1.1X10+00	3.5 1.1X10-06	1.0 Unknown function (adjacent to GAL3)
		APC9	1.9 1.9X10-01	3.8 2.0X10-06	1.2 Component of the anaphase-promoting complex (APC)
		CSG2	0.5 1.9X10+00	3.3 2.4X10-06	1.3 Required for synthesis of the mannosylated sphingolipids
		RPL4B	0.9 1.3X10+00	3.3 2.8X10-06	0.8 Ribosomal protein L4, Gene (adjacent to GAL3)
		YGL132W	0.6 1.8X10+00	3.0 9.1X10-06	1.0 Unknown function, (adjacent to PCL10)
		CHA4	1.5 4.1X10-01	3.1 9.8X10-06	1.0 Zinc-finger protein required for transcriptional activation of CHA1

<1:1 >3/1 >5/1 <1/5 1/1 >5/1

FIGURE 6A

Binding Glucose	Expression (Gal/Glu)	Name	Binding		Expression
			Glucose Ratio p-value	Galactose Ratio p-value	Gal/Glu Ratio
		GAL2	2.8 2.5X10-02	9.5 1.5X10-10	188.6 Galactose permease
		GAL3	1.4 5.4X10-01	8.2 3.5X10-10	18.2 Regulatory protein required for rapid induction of galactose pathway
		GAL7	0.4 2.0X10+00	8.2 6.4X10-10	170.1 UDP-glucose-hexose-1-phosphate uridylyltransferase
		GAL1	1.3 6.0X10-01	7.8 1.5X10-09	271.3 Galactokinase, first step in galactose metabolism
		GAL10	1.3 6.0X10-01	7.8 1.5X10-09	118.8 UDP-glucose 4-epimerase
		FUR4	0.3 2.0X10+00	4.6 4.3X10-08	4.6 Uracil permease (adjacent to GAL1)
		GCY1	0.9 1.2X10+00	4.3 1.3X10-07	93.1 Galactose-induced oxidoreductase
		MTH1	0.9 1.2X10+00	4.0 2.4X10-07	21.6 Repressor of hexose transport genes
		GAL80	0.5 1.9X10+00	3.7 7.0X10-07	4.0 Negative regulator for expression of galactose-induced genes
		PCL10	0.6 1.8X10+00	3.0 8.8X10-06	2.6 Cyclin that associates with Pho85p, involved in glycogen accumulation
		YBR022W	3.7 1.7X10-02	10.4 1.2X10-10	1.5 Unknown function (adjacent to GAL1)
		YDR008C	1.4 5.5X10-01	8.2 3.5X10-10	1.5 Unknown function (share intergenic region with GAL3)
		GIS3	2.7 2.9X10-02	8.0 4.8X10-10	1.0 Multicopy suppressor of the Gal(-) phenotype of snf1 mig1 srb8/10/11 cells
		TLC1	0.6 1.9X10+00	4.2 1.2X10-07	1.0 RNA subunit of telomerase
		PDX3	0.6 1.9X10+00	4.2 1.2X10-07	1.6 Pyridoxine phosphate oxidase
		RIO1	0.9 1.2X10+00	4.3 1.3X10-07	1.4 Unknown function (share intergenic region with GCY1)
		YJR044C	2.3 6.6X10-02	4.0 3.4X10-07	1.7 Unknown function
		SNQ2	0.9 1.1X10+00	3.5 1.1X10-06	0.6 Drug-efflux pump involved in resistance to multiple drugs (adjacent to GAL3)
		YDR010C	0.9 1.1X10+00	3.5 1.1X10-06	1.0 Unknown function (adjacent to GAL3)
		APC9	1.9 1.9X10-01	3.8 2.0X10-06	1.2 Component of the anaphase-promoting complex (APC)
		CSG2	0.5 1.9X10+00	3.3 2.4X10-06	1.3 Required for synthesis of the mannosylated sphingolipids
		RPL48	0.9 1.3X10+00	3.3 2.8X10-06	0.8 Ribosomal protein L4, Gene (adjacent to GAL3)
		YGL132W	0.6 1.8X10+00	3.0 9.1X10-06	1.0 Unknown function, (adjacent to PCL10)
		CHA4	1.5 4.1X10-01	3.1 9.8X10-06	1.0 Zinc-finger protein required for transcriptional activation of CHA1

<1:1 >3/1 >5/1 <1/5 1/1 >5/1

FIGURE 6A

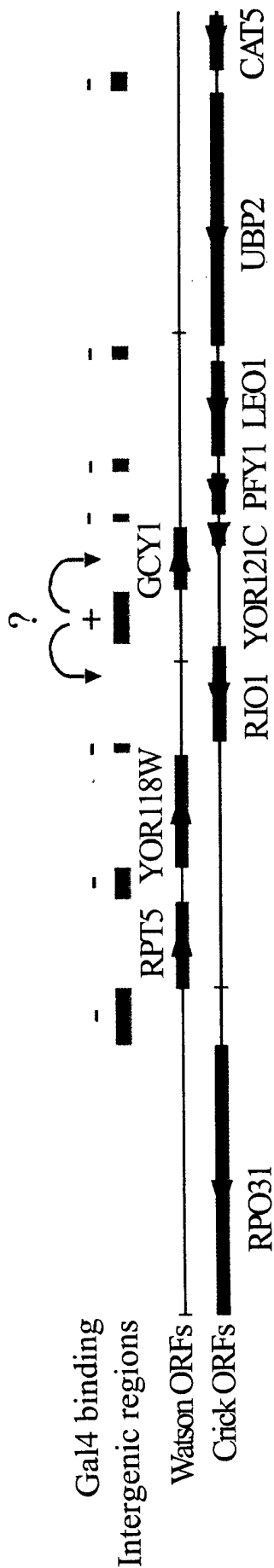


FIGURE 6B

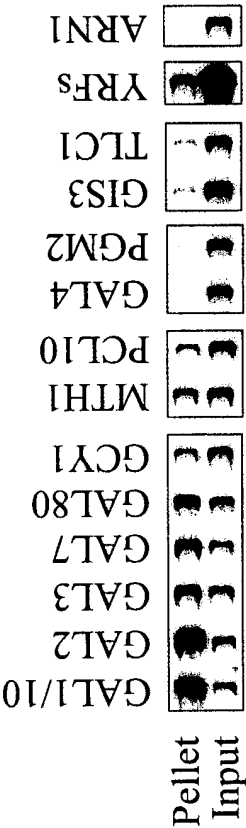


FIGURE 6C

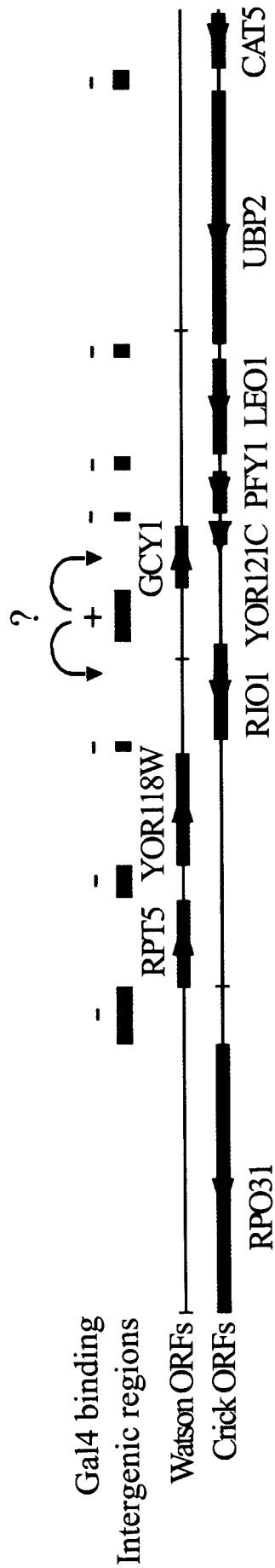


FIGURE 6B

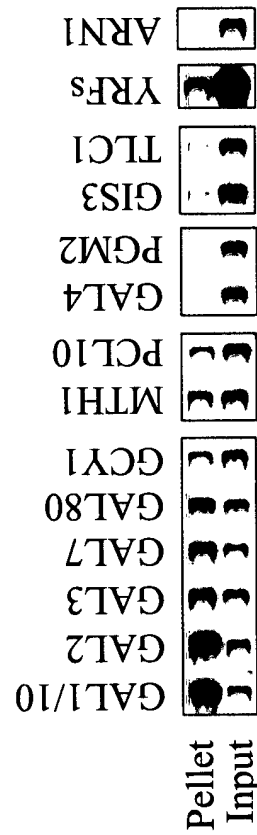


FIGURE 6C

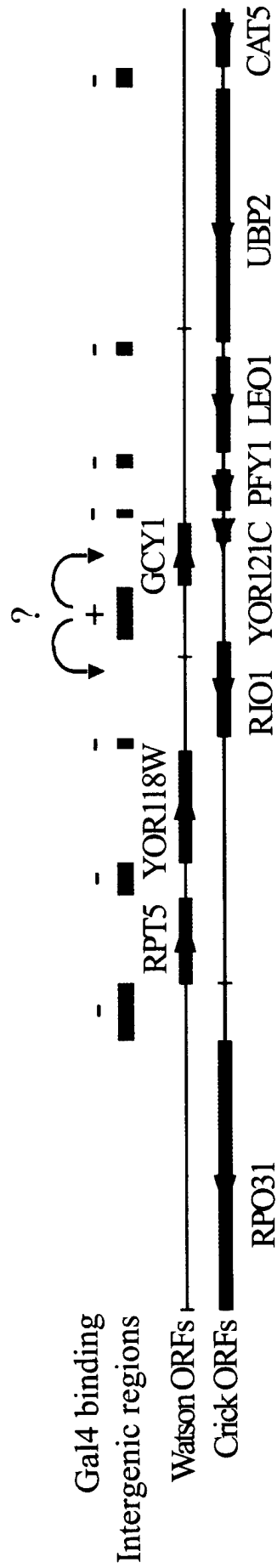


FIGURE 6B

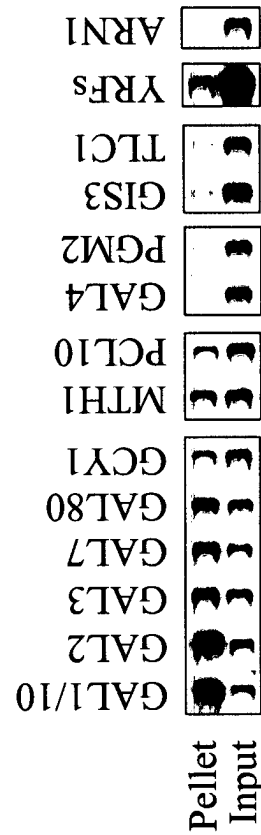


FIGURE 6C

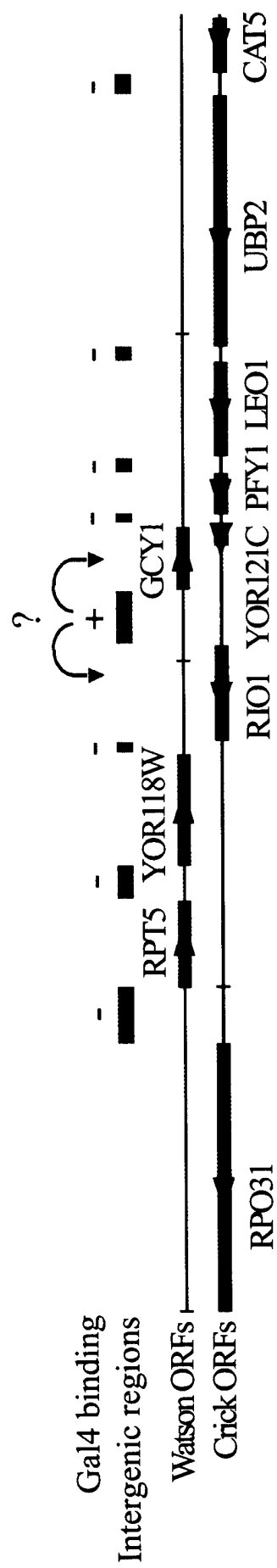


FIGURE 6B

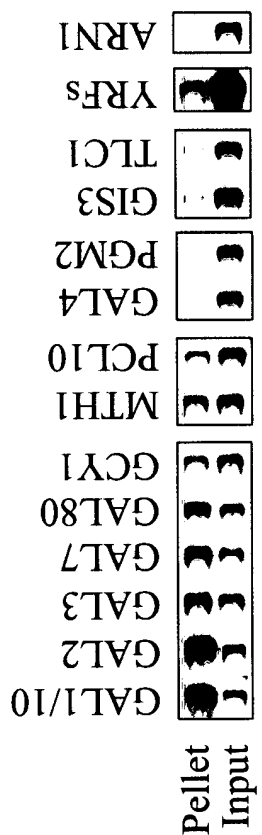


FIGURE 6C

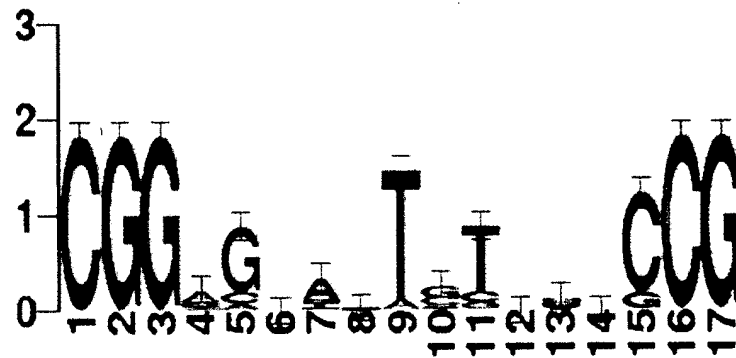


FIGURE 6D

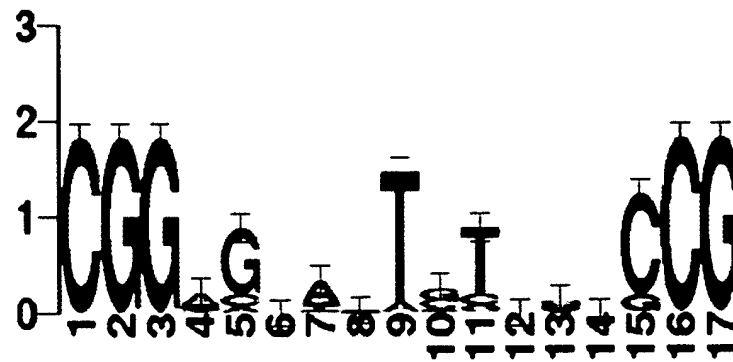


FIGURE 6D

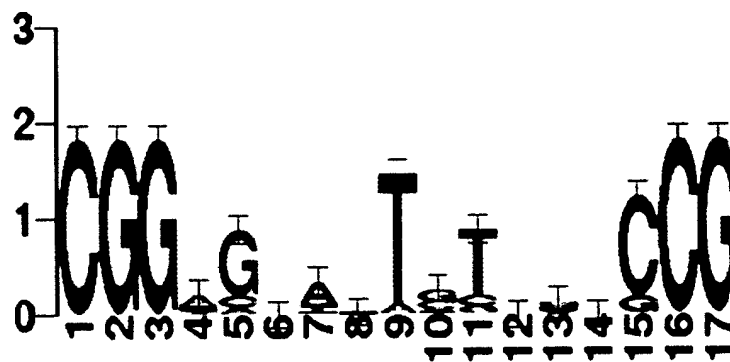


FIGURE 6D

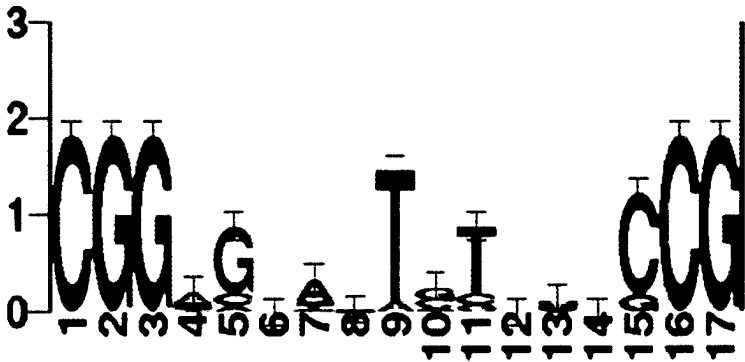


FIGURE 6D

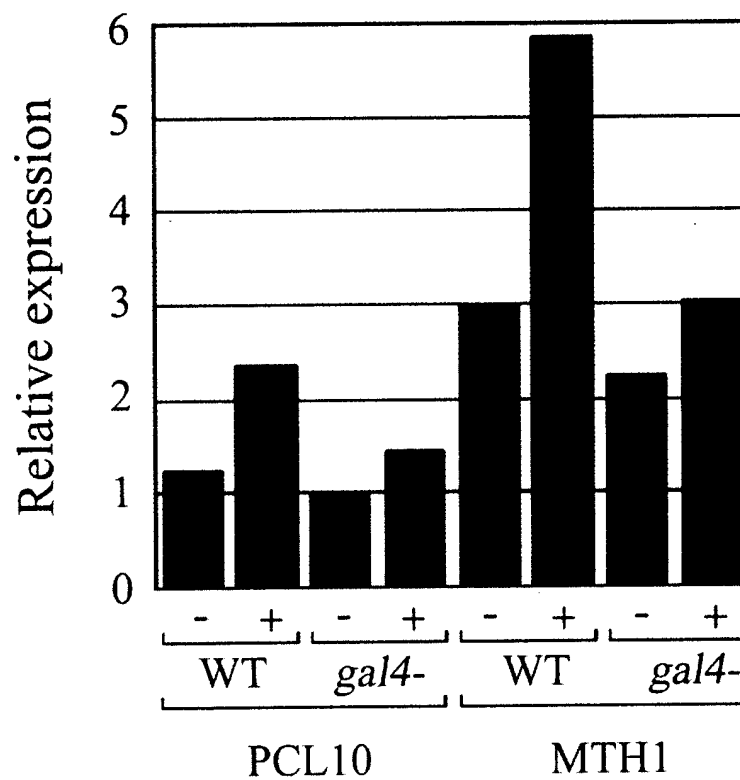


FIGURE 6E

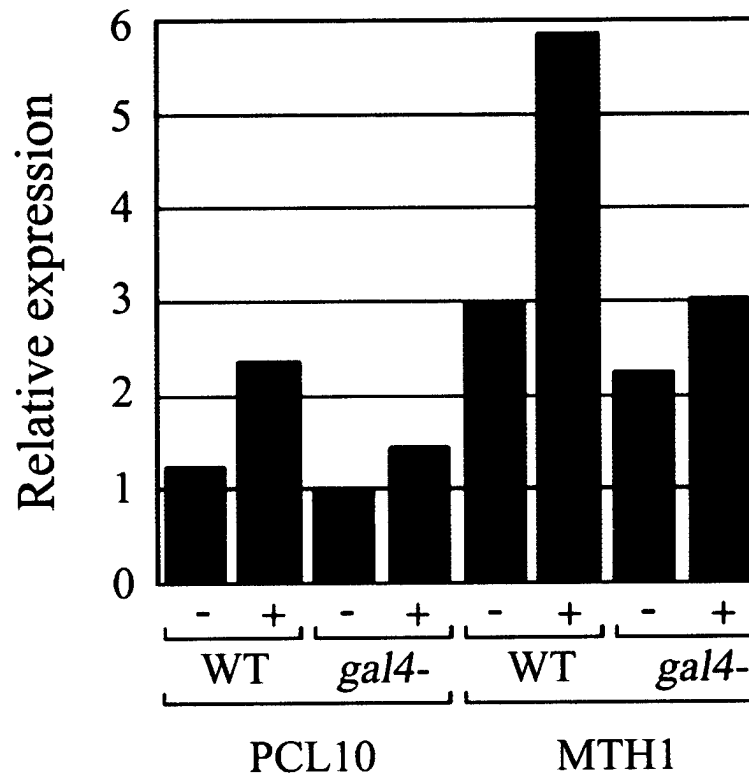


FIGURE 6E

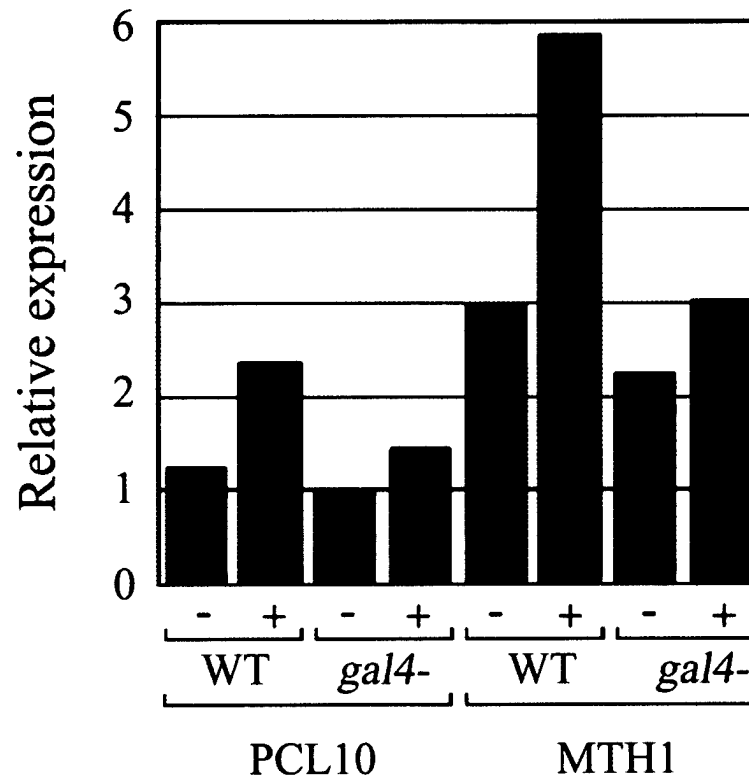


FIGURE 6E



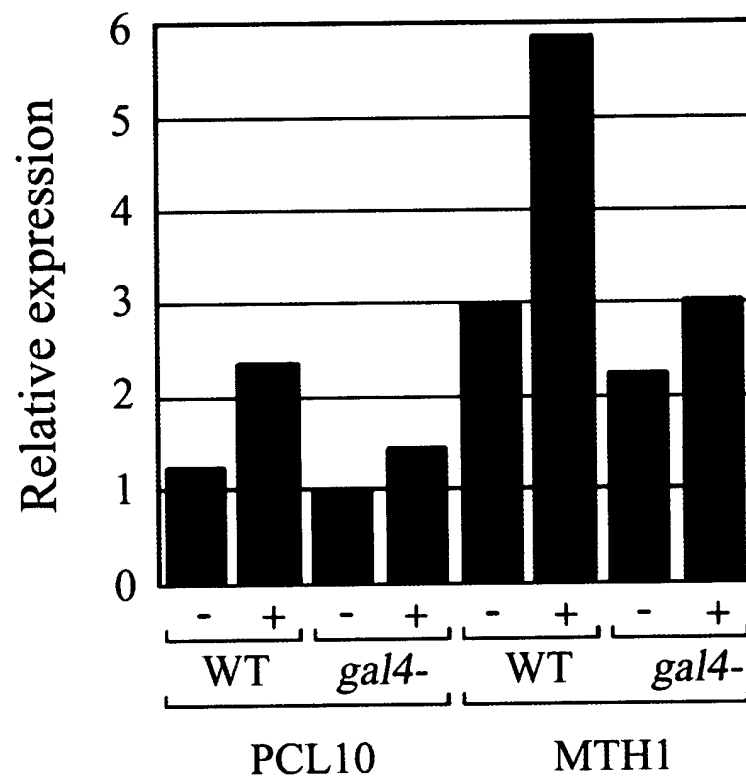


FIGURE 6E



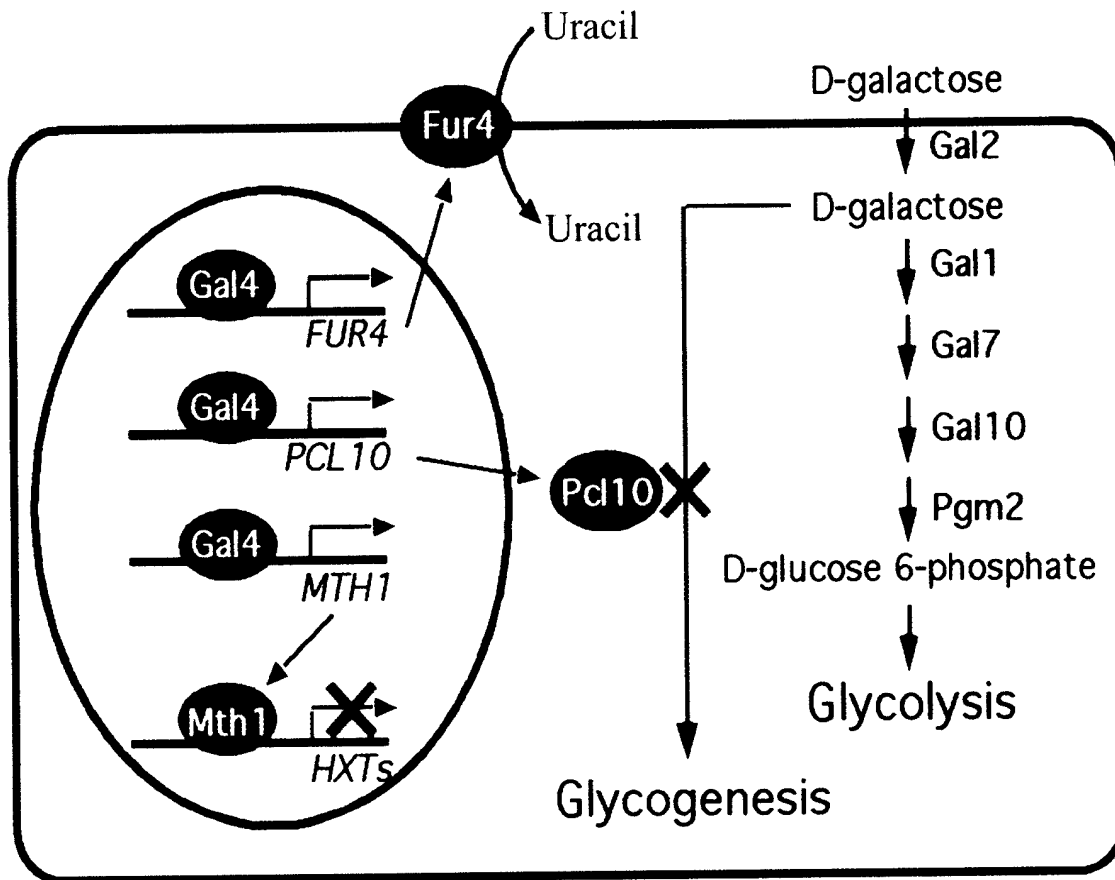


FIGURE 6F

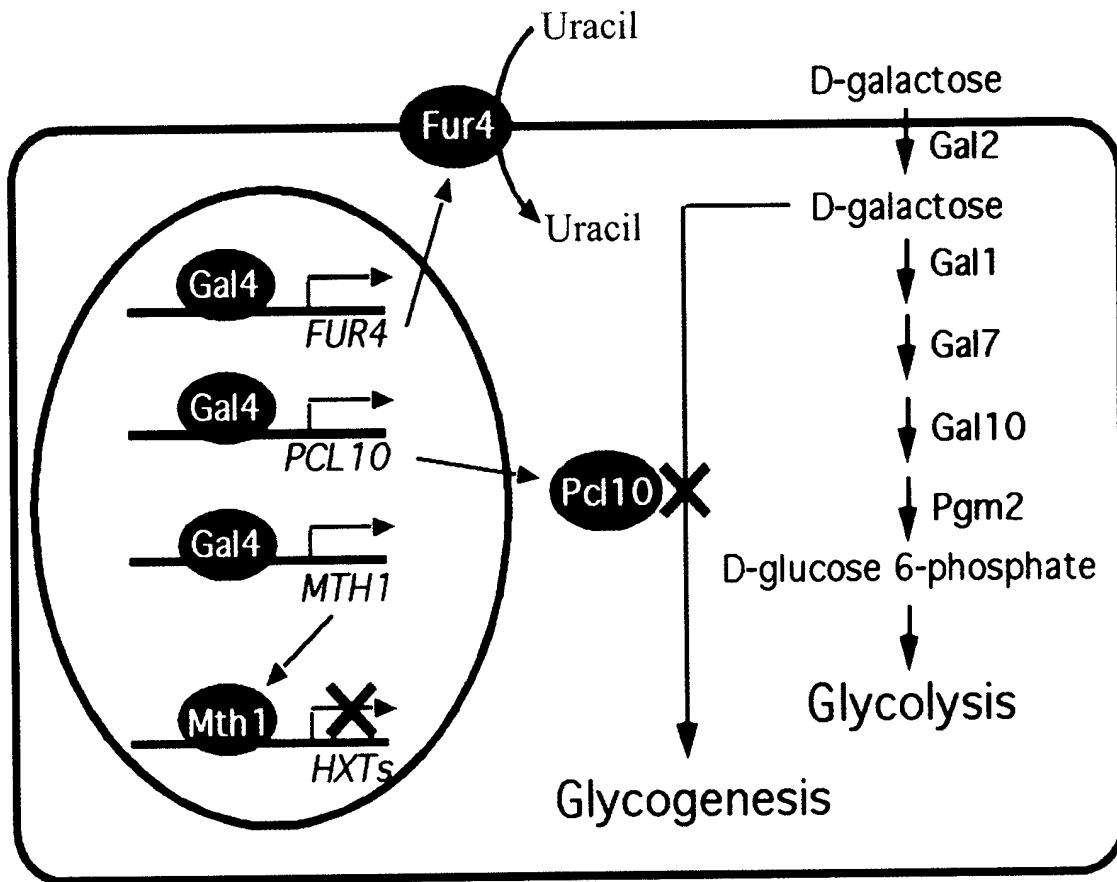


FIGURE 6F

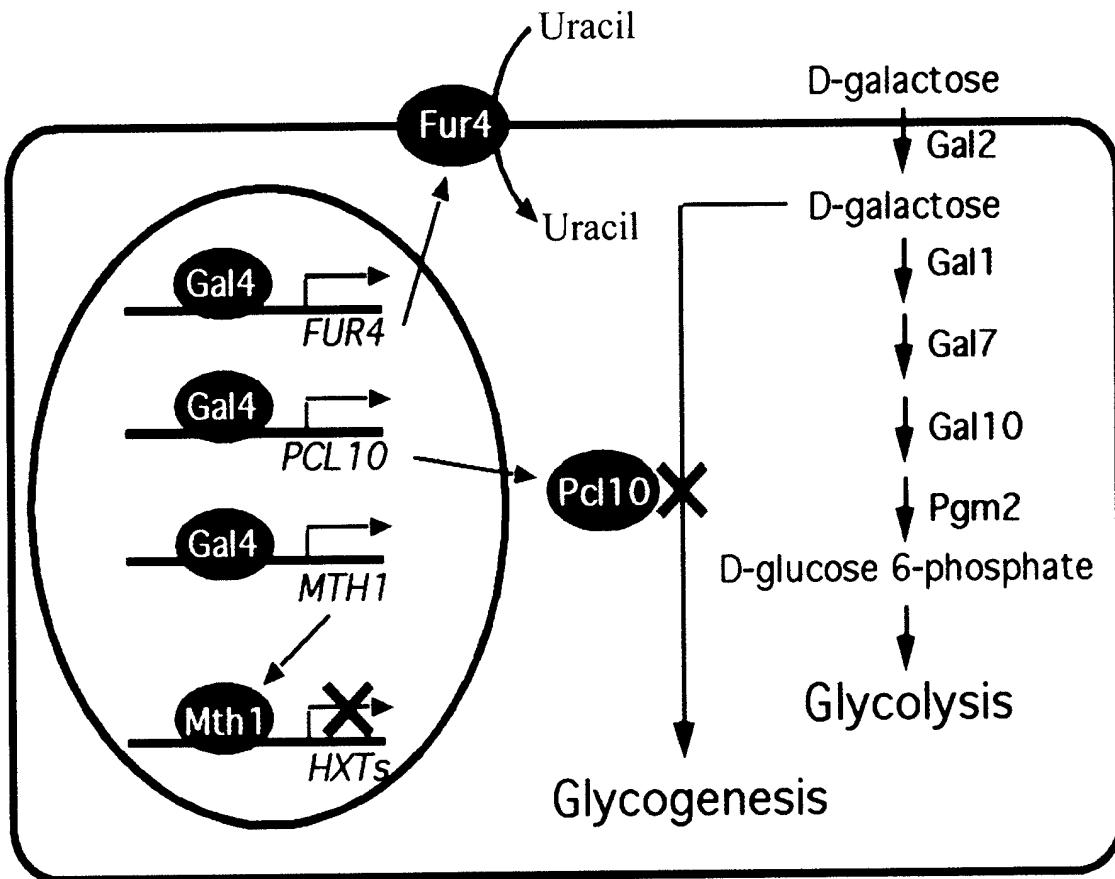


FIGURE 6F

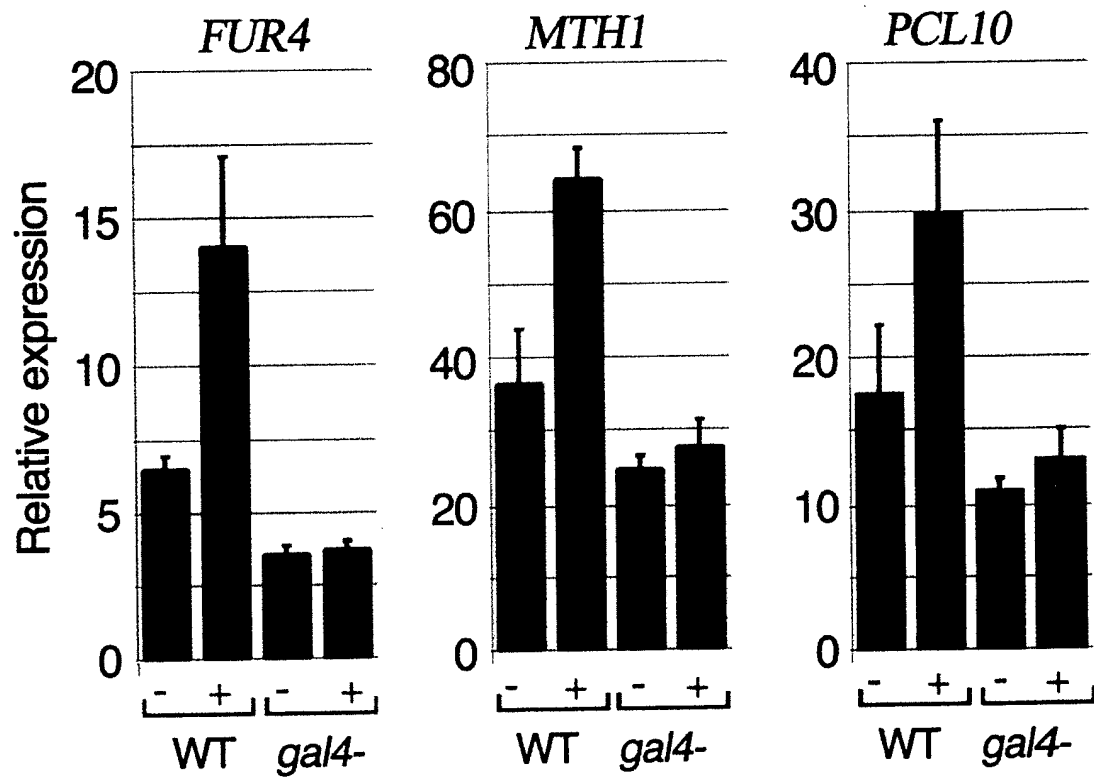


FIGURE 6G

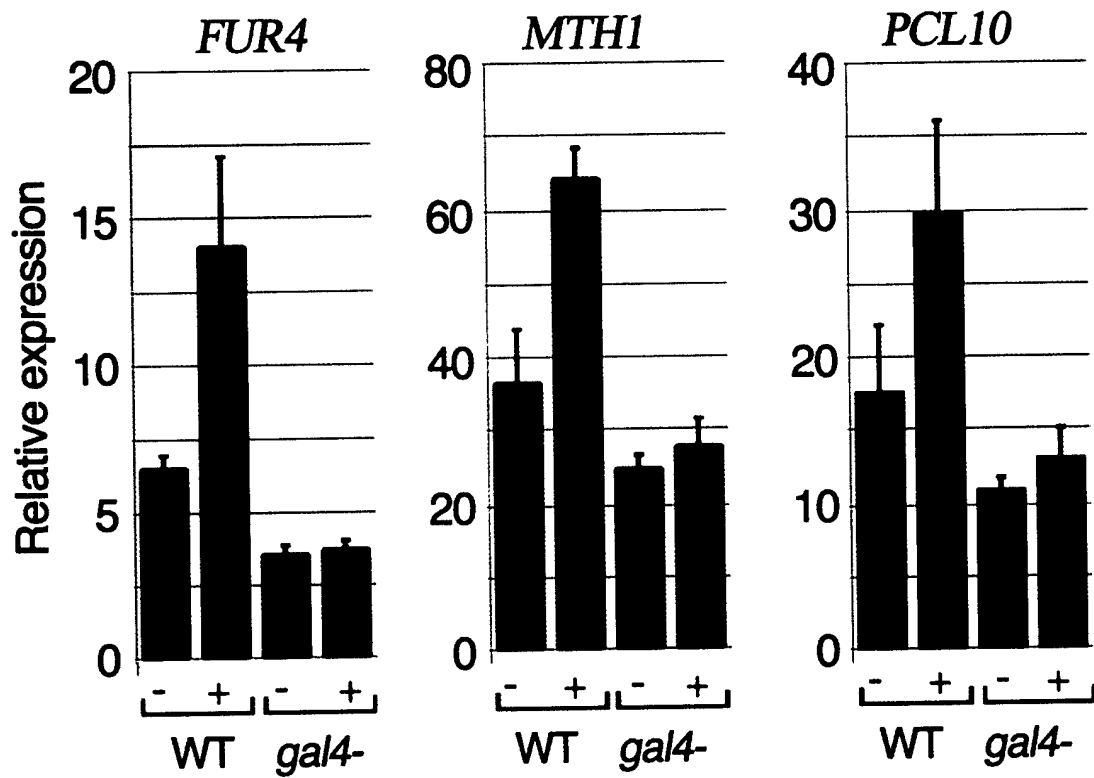


FIGURE 6G

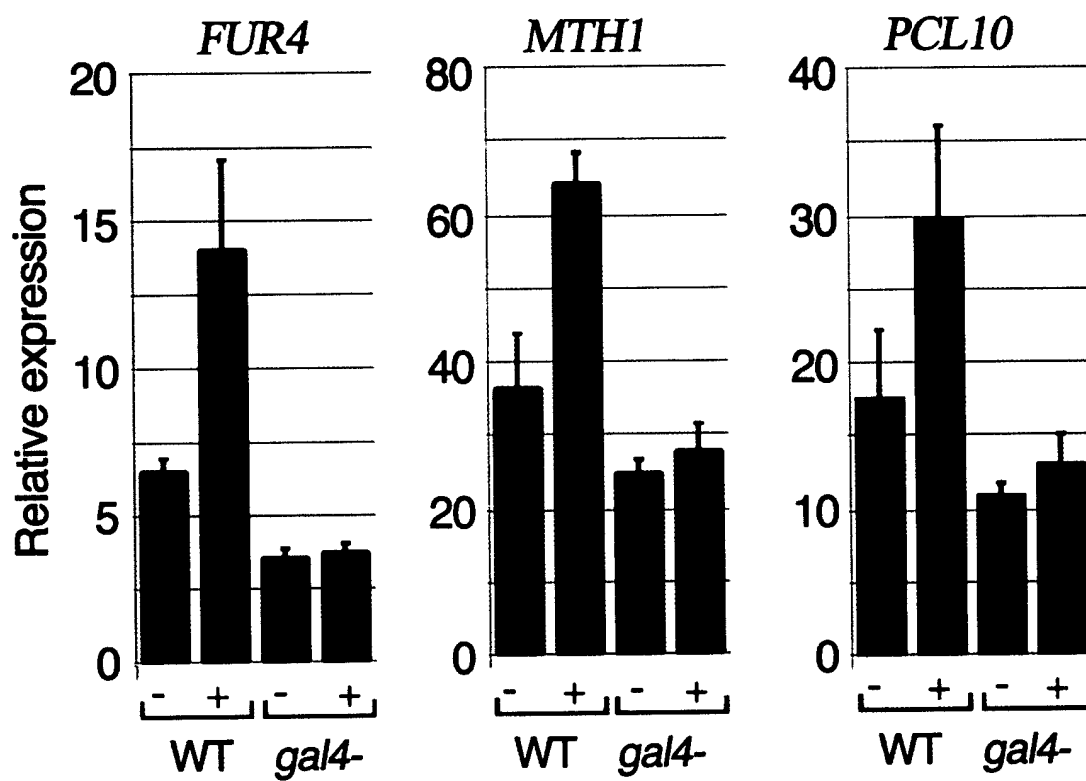


FIGURE 6G



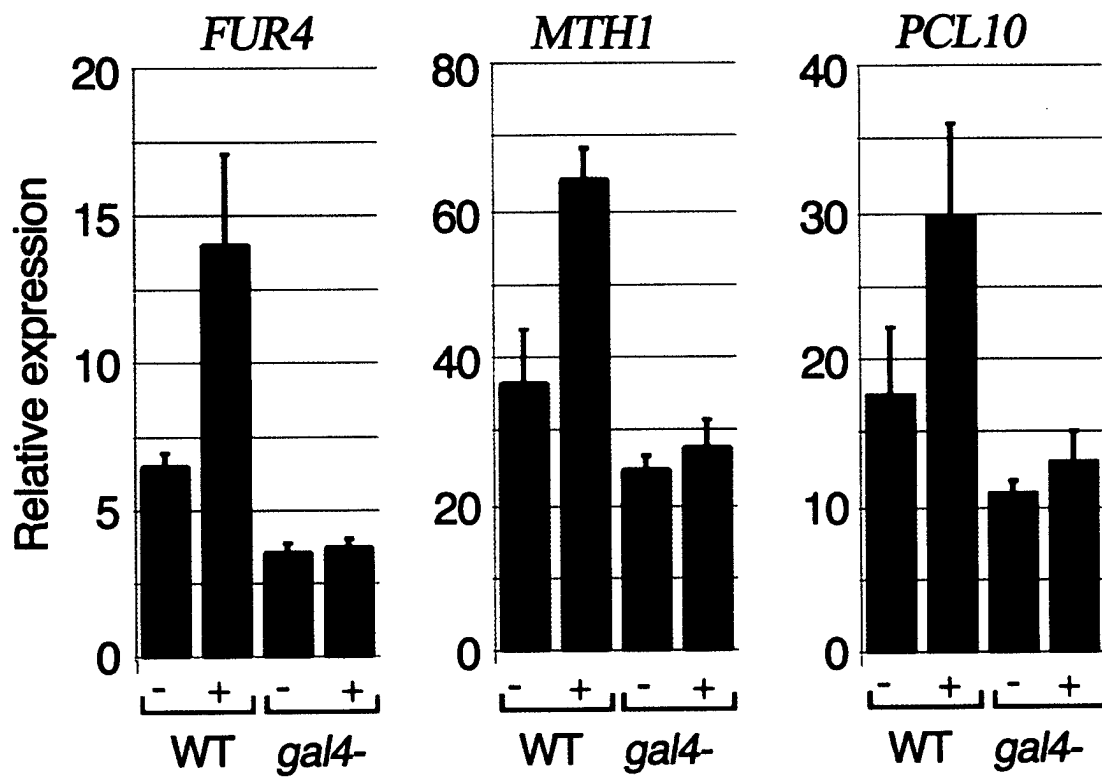


FIGURE 6G

Binding		Expression	Name	Binding		Description		
before	after			before	after			
				ratio	ratio			
			p-value	p-value				
α-0	α-0		PRM1	2.7	1.3E-04	6.2	4.5E-05	Pheromone-regulated membrane protein
α-15	α-15		ERG24	2.7	1.3E-04	6.2	4.5E-05	C-14 sterol reductase
α-30	α-30		PCL2	3.3	4.2E-05	6.8	5.8E-05	Cyclin partly in association with Pho85p
α-45	α-45		FIG2	2.6	2.2E-04	5.6	9.5E-05	Protein involved in mating induction
α-60	α-60		STE12	4.1	1.4E-06	4.1	3.1E-04	Transcription factor required for mating
α-90	α-90		FUS1	5.0	2.8E-07	4.1	5.6E-04	Protein required for cell fusion during mating
α-120	α-120		CDC48	2.9	1.5E-04	4.6	1.0E-03	Required for cell division and homotypic membrane fusion
Gal:Ste12	Gal:Ste12		YCR027C	2.4	5.6E-04	3.2	1.5E-03	Protein involved in growth regulation
Ste12 Δ + α	Ste12 Δ + α		FUS3	3.3	3.9E-05	5.4	2.0E-03	MAPK mediating mating pheromone signaling
			PEP1	3.3	3.9E-05	5.4	2.0E-03	Receptor for vacuolar sorting of soluble vacuolar proteins
			MET2	2.1	4.8E-03	2.8	3.2E-03	Homoserine O-acetyltransferase
			YOR129C	0.7	1.0E+00	5.2	1.0E-04	Protein of unknown function
			UTH1	1.7	2.9E-02	5.2	1.0E-04	Protein involved in the aging process
			AFR1	1.0	8.6E-01	5.1	1.0E-04	Protein involved in morphogenesis of the mating projection
			GIC2	1.4	1.1E-01	5.0	1.2E-04	Putative effector of Cdc42p, important for bud emergence
			YNR046W	1.9	7.6E-03	4.8	1.4E-04	Protein of unknown function
			MSS11	1.0	8.1E-01	4.9	1.8E-04	Protein involved in regulation of starch metabolism
			YOR343C	1.1	7.0E-01	3.9	4.1E-04	Protein of unknown function
			CHS1	0.9	1.0E+00	4.1	4.2E-04	Chitin synthase I, functions during cell separation
			SCH9	1.3	2.1E-01	4.2	4.5E-04	Serine/threonine protein kinase that is activated by cAMP

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FIGURE 7A

Binding	Expression	Name	Binding		Description		
			before	after			
after	before		ratio	ratio	p-value		
		PRM1	2.7	1.3E-04	6.2	4.5E-05	Pheromone-regulated membrane protein
		ERG24	2.7	1.3E-04	6.2	4.5E-05	C-14 sterol reductase
		PCL2	3.3	4.2E-05	6.8	5.8E-05	Cyclin partly in association with Pho85p
		FIG2	2.6	2.2E-04	5.6	9.5E-05	Protein involved in mating induction
		STE12	4.1	1.4E-06	4.1	3.1E-04	Transcription factor required for mating
		FUS1	5.0	2.8E-07	4.1	5.6E-04	Protein required for cell fusion during mating
		CDC48	2.9	1.5E-04	4.6	1.0E-03	Required for cell division and homotypic membrane fusion
		YCR027C	2.4	5.6E-04	3.2	1.5E-03	Protein involved in growth regulation
		FUS3	3.3	3.9E-05	5.4	2.0E-03	MAPK mediating mating pheromone signaling
		PEP1	3.3	3.9E-05	5.4	2.0E-03	Receptor for vacuolar sorting of soluble vacuolar proteins
		MET2	2.1	4.8E-03	2.8	3.2E-03	Homoserine O-acetyltransferase
		YOR129C	0.7	1.0E+00	5.2	1.0E-04	Protein of unknown function
		UTH1	1.7	2.9E-02	5.2	1.0E-04	Protein involved in the aging process
		AFR1	1.0	8.6E-01	5.1	1.0E-04	Protein involved in morphogenesis of the mating projection
		GIC2	1.4	1.1E-01	5.0	1.2E-04	Putative effector of Cdc42p, important for bud emergence
		YNR046W	1.9	7.6E-03	4.8	1.4E-04	Protein of unknown function
		MSS11	1.0	8.1E-01	4.9	1.8E-04	Protein involved in regulation of starch metabolism
		YOR343C	1.1	7.0E-01	3.9	4.1E-04	Protein of unknown function
		CHS1	0.9	1.0E+00	4.1	4.2E-04	Chitin synthase I, functions during cell separation
		SCH9	1.3	2.1E-01	4.2	4.5E-04	Serine/threonine protein kinase that is activated by cAMP

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FIGURE 7A

Binding	Expression	Name	Binding		Description
			before	after	
			ratio p-value	ratio p-value	
		PRM1	2.7 1.3E-04	6.2 4.5E-05	Pheromone-regulated membrane protein
		ERG24	2.7 1.3E-04	6.2 4.5E-05	C-14 sterol reductase
		PCL2	3.3 4.2E-05	6.8 5.8E-05	Cyclin partly in association with Pho85p
		FIG2	2.6 2.2E-04	5.6 9.5E-05	Protein involved in mating induction
		STE12	4.1 1.4E-06	4.1 3.1E-04	Transcription factor required for mating
		FUS1	5.0 2.8E-07	4.1 5.6E-04	Protein required for cell fusion during mating
		CDC48	2.9 1.5E-04	4.6 1.0E-03	Required for cell division and homotypic membrane fusion
		YCR027C	2.4 5.6E-04	3.2 1.5E-03	Protein involved in growth regulation
		FUS3	3.3 3.9E-05	5.4 2.0E-03	MAPK mediating mating pheromone signaling
		PEP1	3.3 3.9E-05	5.4 2.0E-03	Receptor for vacuolar sorting of soluble vacuolar proteins
		MET2	2.1 4.8E-03	2.8 3.2E-03	Homoserine O-acetyltransferase
		YOR129C	0.7 1.0E+00	5.2 1.0E-04	Protein of unknown function
		UTH1	1.7 2.9E-02	5.2 1.0E-04	Protein involved in the aging process
		AFR1	1.0 8.6E-01	5.1 1.0E-04	Protein involved in morphogenesis of the mating projection
		GIC2	1.4 1.1E-01	5.0 1.2E-04	Putative effector of Cdc42p, important for bud emergence
		YNR046W	1.9 7.6E-03	4.8 1.4E-04	Protein of unknown function
		MSS11	1.0 8.1E-01	4.9 1.8E-04	Protein involved in regulation of starch metabolism
		YOR343C	1.1 7.0E-01	3.9 4.1E-04	Protein of unknown function
		CHS1	0.9 1.0E+00	4.1 4.2E-04	Chitin synthase I, functions during cell separation
		SCH9	1.3 2.1E-01	4.2 4.5E-04	Serine/threonine protein kinase that is activated by cAMP

FIGURE 7A

Binding	Expression	Name	Binding		Description		
			before	after			
before	after		ratio	p-value	ratio	p-value	
		PRM1	2.7	1.3E-04	6.2	4.5E-05	Pheromone-regulated membrane protein
		ERG24	2.7	1.3E-04	6.2	4.5E-05	C-14 sterol reductase
		PCL2	3.3	4.2E-05	6.8	5.8E-05	Cyclin partly in association with Pho85p
		FIG2	2.6	2.2E-04	5.6	9.5E-05	Protein involved in mating induction
		STE12	4.1	1.4E-06	4.1	3.1E-04	Transcription factor required for mating
		FUS1	5.0	2.8E-07	4.1	5.6E-04	Protein required for cell fusion during mating
		CDC48	2.9	1.5E-04	4.6	1.0E-03	Required for cell division and homotypic membrane fusion
		YCR027C	2.4	5.6E-04	3.2	1.5E-03	Protein involved in growth regulation
		FUS3	3.3	3.9E-05	5.4	2.0E-03	MAPK mediating mating pheromone signaling
		PEP1	3.3	3.9E-05	5.4	2.0E-03	Receptor for vacuolar sorting of soluble vacuolar proteins
		MET2	2.1	4.8E-03	2.8	3.2E-03	Homoserine O-acetyltransferase
		YOR129C	0.7	1.0E+00	5.2	1.0E-04	Protein of unknown function
		UTH1	1.7	2.9E-02	5.2	1.0E-04	Protein involved in the aging process
		AFR1	1.0	8.6E-01	5.1	1.0E-04	Protein involved in morphogenesis of the mating projection
		GIC2	1.4	1.1E-01	5.0	1.2E-04	Putative effector of Cdc42p, important for bud emergence
		YNR046W	1.9	7.6E-03	4.8	1.4E-04	Protein of unknown function
		MSS11	1.0	8.1E-01	4.9	1.8E-04	Protein involved in regulation of starch metabolism
	YOR343C	1.1	7.0E-01	3.9	4.1E-04	Protein of unknown function	
	CHS1	0.9	1.0E+00	4.1	4.2E-04	Chitin synthase I, functions during cell separation	
	SCH9	1.3	2.1E-01	4.2	4.5E-04	Serine/threonine protein kinase that is activated by cAMP	

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FIGURE 7A

Binding	Expression	Name	Binding		Description		
			before	after			
before	after		ratio	p-value	ratio	p-value	
α-0	α-15	KAR5	1.2	3.7E-01	3.8	4.7E-04	Membrane protein required for homotypic nuclear fusion
α-30	α-60	YER048W-A	1.5	1.0E-01	3.8	5.1E-04	Protein of unknown function
α-90	α-120	YPL192C	0.9	1.0E+00	3.6	6.5E-04	Protein of unknown function
Gal:Ste12	Ste12Δ	SPC25	1.3	2.0E-01	4.1	6.6E-04	Protein of the spindle pole body
Ste12Δ + α		YER019W	1.3	2.0E-01	4.1	6.6E-04	Moderately similar to mammalian neutral sphingomyelinases
		YIL083C	1.0	6.7E-01	3.6	7.1E-04	Protein of unknown function
		PGM1	2.0	6.1E-03	3.8	7.2E-04	Phosphoglucosyltransferase
		YIL037C	1.1	5.5E-01	3.4	8.2E-04	Protein of unknown function
		YIL169C	1.6	7.2E-02	3.3	1.2E-03	Protein of unknown function
		AGA1	1.4	1.1E-01	3.1	1.9E-03	α-Agglutinin anchor subunit
		YOL155C	1.0	7.3E-01	3.0	2.1E-03	Similar to <i>S. cerevisiae</i> glucan 1,4-α-glucosidase
		VTI1	0.9	1.0E+00	3.0	2.2E-03	Synaptobrevin (v-SNARE) homolog
		CIK1	0.9	1.0E+00	3.0	2.2E-03	Involved in spindle formation and karyogamy
		FAR1	1.3	2.2E-01	3.0	2.4E-03	Involved in cell cycle arrest for mating
		PHO81	1.0	8.3E-01	2.9	2.7E-03	CDK inhibitor for Pho80p-Pho85p complex
		YNR064C	1.5	7.4E-02	2.7	4.5E-03	Similar to <i>Rhodobacter capsulatus</i> bchO protein
		HYM1	1.4	1.8E-01	2.7	4.9E-03	Protein with similarity to <i>Aspergillus nidulans</i> hymA
		FIG1	1.2	3.8E-01	2.9	5.0E-03	Protein required for efficient mating

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FIGURE 7B

Binding	Expression	Name	Binding		Description		
			before	after			
before	after		ratio	p-value	ratio	p-value	
0	0	KAR5	1.2	3.7E-01	3.8	4.7E-04	Membrane protein required for homotypic nuclear fusion
0	0	YER048W-A	1.5	1.0E-01	3.8	5.1E-04	Protein of unknown function
0	0	YPL192C	0.9	1.0E+00	3.6	6.5E-04	Protein of unknown function
0	0	SPC25	1.3	2.0E-01	4.1	6.6E-04	Protein of the spindle pole body
0	0	YER019W	1.3	2.0E-01	4.1	6.6E-04	Moderately similar to mammalian neutral sphingomyelinases
0	0	YIL083C	1.0	6.7E-01	3.6	7.1E-04	Protein of unknown function
0	0	PGM1	2.0	6.1E-03	3.8	7.2E-04	Phosphoglucosyltransferase
0	0	YIL037C	1.1	5.5E-01	3.4	8.2E-04	Protein of unknown function
0	0	YIL169C	1.6	7.2E-02	3.3	1.2E-03	Protein of unknown function
0	0	AGA1	1.4	1.1E-01	3.1	1.9E-03	a-Agglutinin anchor subunit
0	0	YOL155C	1.0	7.3E-01	3.0	2.1E-03	Similar to <i>S. cerevisiae</i> glucan 1,4-alpha-glucosidase
0	0	VTI1	0.9	1.0E+00	3.0	2.2E-03	Synaptobrevin (v-SNARE) homolog
0	0	CIK1	0.9	1.0E+00	3.0	2.2E-03	Involved in spindle formation and karyogamy
0	0	FAR1	1.3	2.2E-01	3.0	2.4E-03	Involved in cell cycle arrest for mating
0	0	PHO81	1.0	8.3E-01	2.9	2.7E-03	CDK inhibitor for Pho80p-Pho85p complex
0	0	YNR064C	1.5	7.4E-02	2.7	4.5E-03	Similar to <i>Rhodobacter capsulatus</i> bchO protein
0	0	HYM1	1.4	1.8E-01	2.7	4.9E-03	Protein with similarity to <i>Aspergillus nidulans</i> hymA
0	0	FIG1	1.2	3.8E-01	2.9	5.0E-03	Protein required for efficient mating

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FIGURE 7B

Binding	Expression	Name	Binding		Description																																																																																																																																											
			before	after																																																																																																																																												
after	before		ratio	p-value																																																																																																																																												
<div>after</div> <div>before</div> <div>after</div> <div>before</div> <div>after</div> <div>before</div> <div>after</div> <div>before</div> <div>after</div> <div>before</div> <div>after</div> <div>before</div> <div>after</div> <div>before</div> <div>after</div> <div>before</div> <div>after</div> <div>before</div> <tr><td></td><td></td><td>KAR5</td><td>1.2</td><td>3.7E-01</td><td>3.8</td><td>4.7E-04</td><td>Membrane protein required for homotypic nuclear fusion</td></tr> <tr><td></td><td></td><td>YER048W-A</td><td>1.5</td><td>1.0E-01</td><td>3.8</td><td>5.1E-04</td><td>Protein of unknown function</td></tr> <tr><td></td><td></td><td>YPL192C</td><td>0.9</td><td>1.0E+00</td><td>3.6</td><td>6.5E-04</td><td>Protein of unknown function</td></tr> <tr><td></td><td></td><td>SPC25</td><td>1.3</td><td>2.0E-01</td><td>4.1</td><td>6.6E-04</td><td>Protein of the spindle pole body</td></tr> <tr><td></td><td></td><td>YER019W</td><td>1.3</td><td>2.0E-01</td><td>4.1</td><td>6.6E-04</td><td>Moderately similar to mammalian neutral sphingomyelinases</td></tr> <tr><td></td><td></td><td>YIL083C</td><td>1.0</td><td>6.7E-01</td><td>3.6</td><td>7.1E-04</td><td>Protein of unknown function</td></tr> <tr><td></td><td></td><td>PGM1</td><td>2.0</td><td>6.1E-03</td><td>3.8</td><td>7.2E-04</td><td>Phosphoglucomutase</td></tr> <tr><td></td><td></td><td>YIL037C</td><td>1.1</td><td>5.5E-01</td><td>3.4</td><td>8.2E-04</td><td>Protein of unknown function</td></tr> <tr><td></td><td></td><td>YIL169C</td><td>1.6</td><td>7.2E-02</td><td>3.3</td><td>1.2E-03</td><td>Protein of unknown function</td></tr> <tr><td></td><td></td><td>AGA1</td><td>1.4</td><td>1.1E-01</td><td>3.1</td><td>1.9E-03</td><td>α-Agglutinin anchor subunit</td></tr> <tr><td></td><td></td><td>YOL155C</td><td>1.0</td><td>7.3E-01</td><td>3.0</td><td>2.1E-03</td><td>Similar to <i>S. cerevisiae</i> glucan 1,4-alpha-glucosidase</td></tr> <tr><td></td><td></td><td>VTI1</td><td>0.9</td><td>1.0E+00</td><td>3.0</td><td>2.2E-03</td><td>Synaptobrevin (v-SNARE) homolog</td></tr> <tr><td></td><td></td><td>CIK1</td><td>0.9</td><td>1.0E+00</td><td>3.0</td><td>2.2E-03</td><td>Involved in spindle formation and karyogamy</td></tr> <tr><td></td><td></td><td>FAR1</td><td>1.3</td><td>2.2E-01</td><td>3.0</td><td>2.4E-03</td><td>Involved in cell cycle arrest for mating</td></tr> <tr><td></td><td></td><td>PHO81</td><td>1.0</td><td>8.3E-01</td><td>2.9</td><td>2.7E-03</td><td>CDK inhibitor for Pho80p-Pho85p complex</td></tr> <tr><td></td><td></td><td>YNR064C</td><td>1.5</td><td>7.4E-02</td><td>2.7</td><td>4.5E-03</td><td>Similar to <i>Rhodobacter capsulatus</i> bchO protein</td></tr> <tr><td></td><td></td><td>HYM1</td><td>1.4</td><td>1.8E-01</td><td>2.7</td><td>4.9E-03</td><td>Protein with similarity to <i>Aspergillus nidulans</i> hymA</td></tr> <tr><td></td><td></td><td>FIG1</td><td>1.2</td><td>3.8E-01</td><td>2.9</td><td>5.0E-03</td><td>Protein required for efficient mating</td></tr>			KAR5	1.2	3.7E-01	3.8	4.7E-04	Membrane protein required for homotypic nuclear fusion			YER048W-A	1.5	1.0E-01	3.8	5.1E-04	Protein of unknown function			YPL192C	0.9	1.0E+00	3.6	6.5E-04	Protein of unknown function			SPC25	1.3	2.0E-01	4.1	6.6E-04	Protein of the spindle pole body			YER019W	1.3	2.0E-01	4.1	6.6E-04	Moderately similar to mammalian neutral sphingomyelinases			YIL083C	1.0	6.7E-01	3.6	7.1E-04	Protein of unknown function			PGM1	2.0	6.1E-03	3.8	7.2E-04	Phosphoglucomutase			YIL037C	1.1	5.5E-01	3.4	8.2E-04	Protein of unknown function			YIL169C	1.6	7.2E-02	3.3	1.2E-03	Protein of unknown function			AGA1	1.4	1.1E-01	3.1	1.9E-03	α -Agglutinin anchor subunit			YOL155C	1.0	7.3E-01	3.0	2.1E-03	Similar to <i>S. cerevisiae</i> glucan 1,4-alpha-glucosidase			VTI1	0.9	1.0E+00	3.0	2.2E-03	Synaptobrevin (v-SNARE) homolog			CIK1	0.9	1.0E+00	3.0	2.2E-03	Involved in spindle formation and karyogamy			FAR1	1.3	2.2E-01	3.0	2.4E-03	Involved in cell cycle arrest for mating			PHO81	1.0	8.3E-01	2.9	2.7E-03	CDK inhibitor for Pho80p-Pho85p complex			YNR064C	1.5	7.4E-02	2.7	4.5E-03	Similar to <i>Rhodobacter capsulatus</i> bchO protein			HYM1	1.4	1.8E-01	2.7	4.9E-03	Protein with similarity to <i>Aspergillus nidulans</i> hymA			FIG1	1.2	3.8E-01	2.9	5.0E-03	Protein required for efficient mating
			KAR5	1.2	3.7E-01	3.8	4.7E-04	Membrane protein required for homotypic nuclear fusion																																																																																																																																								
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			YPL192C	0.9	1.0E+00	3.6	6.5E-04	Protein of unknown function																																																																																																																																								
			SPC25	1.3	2.0E-01	4.1	6.6E-04	Protein of the spindle pole body																																																																																																																																								
			YER019W	1.3	2.0E-01	4.1	6.6E-04	Moderately similar to mammalian neutral sphingomyelinases																																																																																																																																								
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			PGM1	2.0	6.1E-03	3.8	7.2E-04	Phosphoglucomutase																																																																																																																																								
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			FAR1	1.3	2.2E-01	3.0	2.4E-03	Involved in cell cycle arrest for mating																																																																																																																																								
			PHO81	1.0	8.3E-01	2.9	2.7E-03	CDK inhibitor for Pho80p-Pho85p complex																																																																																																																																								
			YNR064C	1.5	7.4E-02	2.7	4.5E-03	Similar to <i>Rhodobacter capsulatus</i> bchO protein																																																																																																																																								
			HYM1	1.4	1.8E-01	2.7	4.9E-03	Protein with similarity to <i>Aspergillus nidulans</i> hymA																																																																																																																																								
		FIG1	1.2	3.8E-01	2.9	5.0E-03	Protein required for efficient mating																																																																																																																																									

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>10/1

4/1

5/1

3/1

2/1

1/1

1/2

1/5

<1/10

FIGURE 7B

Binding	Expression	Name	Binding		Description		
			before	after			
before	after		ratio	p-value			
α-0 α-15 α-30 α-45 α-60 α-75 α-90 α-120 Gal:Ste12 Ste12Δ Ste12Δ + α		KAR5	1.2	3.7E-01	3.8	4.7E-04	Membrane protein required for homotypic nuclear fusion
		YER048W-A	1.5	1.0E-01	3.8	5.1E-04	Protein of unknown function
		YPL192C	0.9	1.0E+00	3.6	6.5E-04	Protein of unknown function
		SPC25	1.3	2.0E-01	4.1	6.6E-04	Protein of the spindle pole body
		YER019W	1.3	2.0E-01	4.1	6.6E-04	Moderately similar to mammalian neutral sphingomyelinases
		YIL083C	1.0	6.7E-01	3.6	7.1E-04	Protein of unknown function
		PGM1	2.0	6.1E-03	3.8	7.2E-04	Phosphoglucomutase
		YIL037C	1.1	5.5E-01	3.4	8.2E-04	Protein of unknown function
		YIL169C	1.6	7.2E-02	3.3	1.2E-03	Protein of unknown function
		AGA1	1.4	1.1E-01	3.1	1.9E-03	α-Agglutinin anchor subunit
		YOL155C	1.0	7.3E-01	3.0	2.1E-03	Similar to S. cerevisiae glucan 1,4-α-glucosidase
		VTI1	0.9	1.0E+00	3.0	2.2E-03	Synaptobrevin (v-SNARE) homolog
		CIK1	0.9	1.0E+00	3.0	2.2E-03	Involved in spindle formation and karyogamy
		FAR1	1.3	2.2E-01	3.0	2.4E-03	Involved in cell cycle arrest for mating
		PHO81	1.0	8.3E-01	2.9	2.7E-03	CDK inhibitor for Pho80p-Pho85p complex
		YNR064C	1.5	7.4E-02	2.7	4.5E-03	Similar to Rhodobacter capsulatus bchO protein
		HYM1	1.4	1.8E-01	2.7	4.9E-03	Protein with similarity to Aspergillus nidulans hymA
		FIG1	1.2	3.8E-01	2.9	5.0E-03	Protein required for efficient mating

>5/1

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1/1

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1/5

<1/10

FIGURE 7B

Binding	Expression	Name	Binding		ratio p-value	p-value	Description
			before	after			
before	after						
0	15						
15	30						
30	45						
45	60						
60	75						
75	90						
90	120						
Gal:Ste12	Ste12Δ + α						
		BMH2	2.1	3.2E-03	4.1	6.5E-04	Homolog to 14-3-3 protein; adjacent to Ty element YDRCdelta9
		YGR189C	1.7	2.4E-02	4.8	1.7E-04	Cell wall protein; adjacent to Ty element YGRWdelta31
		YNR053C	1.9	9.7E-03	4.3	2.6E-04	Unknown function; adjacent to Ty element YNRWsigma4
		MSO1	1.9	1.8E-02	4.3	2.9E-04	Multicopy suppressor of sec1; adjacent to Ty element YNRWsigma4
		TYE7	1.0	1.0E+00	3.9	4.6E-04	Basic helix-loop-helix transcription factor
		YNR051C	1.8	1.4E-02	3.8	4.7E-04	Similar to chicken nucleolin; adjacent to Ty element YNRWsigma4
		YNR048W	1.9	9.2E-03	3.9	4.9E-04	Protein of unknown function; adjacent to Ty element YNRWsigma4
		YGL050W	1.7	2.0E-02	3.8	5.1E-04	Protein of unknown function; adjacent to Ty element YGLCsigma3
		YIL036W	1.1	5.5E-01	3.4	8.2E-04	Similar to Mei4p and to CREB proteins; adjacent to YIL037C
		YNR067C	2.0	1.3E-02	3.4	1.1E-03	Protein of unknown function
		SDL1	1.6	7.2E-02	3.3	1.2E-03	Serine dehydratase; adjacent to YIL169C
		YDR281C	1.2	4.2E-01	3.1	1.7E-03	Protein of unknown function; adjacent to Ty element YDRWsigma5
		YDR100W	1.1	3.6E-01	5.5	1.9E-03	Protein of unknown function; adjacent to Ty element YDRCdelta9
		YNL043C	1.1	5.7E-01	3.0	2.1E-03	Protein of unknown function; adjacent to Ty element YNLWsigma2
		YOL154W	1.0	7.3E-01	3.0	2.1E-03	Similar to Zinc metalloproteinases; adjacent to YOL155C
		YHB1	1.0	8.3E-01	2.9	2.7E-03	Flavohemoglobin of unknown function; adjacent to PHO81
		PAN3	1.8	6.5E-02	4.6	3.5E-03	Component of Pab1p-stimulated poly(A) ribonuclease
		CWP2	1.8	1.5E-02	2.8	3.6E-03	major constituent of the cell wall containing GPI-anchor
		YKL097C	1.8	1.5E-02	2.8	3.6E-03	Protein of unknown function; adjacent to CWP2

>5/1 4/1 3/1 2/1 <1:1 >10/1 5/1 2/1 1:1 1/2 1/5 <1/10

FIGURE 7C

Binding	Expression	Name	Binding		Description
			before	after	
			ratio	p-value	
		BMH2	2.1	3.2E-03	4.1 6.5E-04 Homolog to 14-3-3 protein; adjacent to Ty element YDRCDelta9
		YGR189C	1.7	2.4E-02	4.8 1.7E-04 Cell wall protein; adjacent to TY element YGRWDelta31
		YNR053C	1.9	9.7E-03	4.3 2.6E-04 Unknown function; adjacent to Ty element YNRWsigma4
		MSO1	1.9	1.8E-02	4.3 2.9E-04 Multicopy suppressor of sec1; adjacent to Ty element YNRWsigma4
		TYE7	1.0	1.0E+00	3.9 4.6E-04 Basic helix-loop-helix transcription factor
		YNR051C	1.8	1.4E-02	3.8 4.7E-04 Similar to chicken nucleolin; adjacent to Ty element YNRWsigma4
		YNR048W	1.9	9.2E-03	3.9 4.9E-04 Protein of unknown function; adjacent to Ty element YNRWsigma4
		YGL050W	1.7	2.0E-02	3.8 5.1E-04 Protein of unknown function; adjacent to Ty element YGLCsigma3
		YIL036W	1.1	5.5E-01	3.4 8.2E-04 Similar to Mei4p and to CREB proteins; adjacent to YIL037C
		YNR067C	2.0	1.3E-02	3.4 1.1E-03 Protein of unknown function
		SDL1	1.6	7.2E-02	3.3 1.2E-03 Serine dehydratase; adjacent to YIL169C
		YDR281C	1.2	4.2E-01	3.1 1.7E-03 Protein of unknown function; adjacent to Ty element YDRWsigma5
		YDR100W	1.1	3.6E-01	5.5 1.9E-03 Protein of unknown function; adjacent to Ty element YDRCDelta9
		YNL043C	1.1	5.7E-01	3.0 2.1E-03 Protein of unknown function; adjacent to Ty element YNLWsigma2
		YOL154W	1.0	7.3E-01	3.0 2.1E-03 Similar to Zinc metalloproteinases; adjacent to YOL155C
		YHB1	1.0	8.3E-01	2.9 2.7E-03 Flavohemoglobin of unknown function; adjacent to PHO81
		PAN3	1.8	6.5E-02	4.6 3.5E-03 Component of Pab1p-stimulated poly(A) ribonuclease
		CWP2	1.8	1.5E-02	2.8 3.6E-03 major constituent of the cell wall containing GPI-anchor
		YKL097C	1.8	1.5E-02	2.8 3.6E-03 Protein of unknown function; adjacent to CWP2

FIGURE 7C

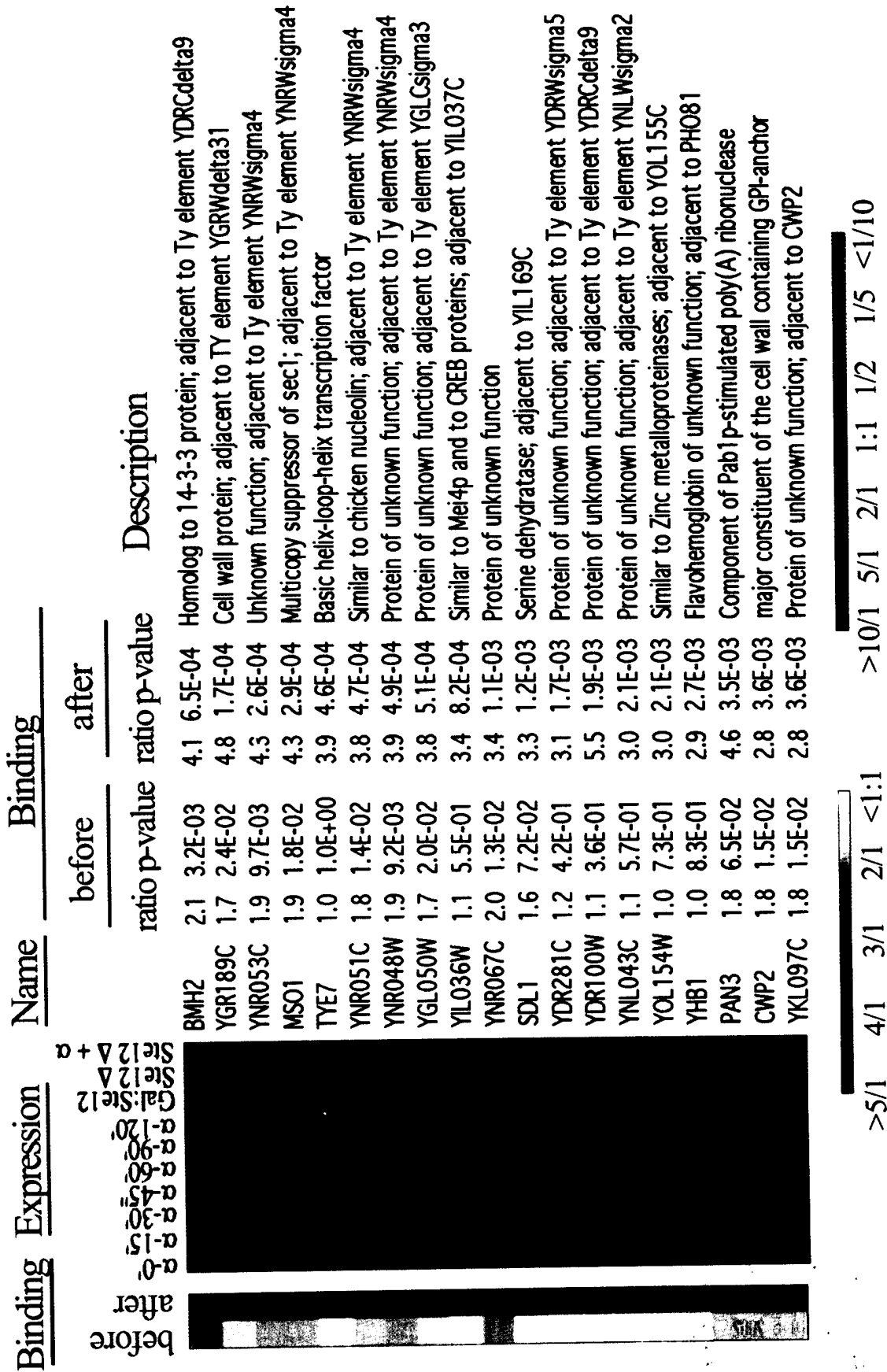


FIGURE 7C

Binding	Expression	Name	Binding		ratio	p-value	ratio	p-value	Description
			before	after					
before	after								
0	0	BMH2	2.1	3.2E-03	4.1	6.5E-04	Homolog to 14-3-3 protein; adjacent to Ty element YDRCdelta9		
0	0	YGR189C	1.7	2.4E-02	4.8	1.7E-04	Cell wall protein; adjacent to TY element YGRWdelta31		
0	0	YNR053C	1.9	9.7E-03	4.3	2.6E-04	Unknown function; adjacent to Ty element YNRWsigma4		
0	0	MSO1	1.9	1.8E-02	4.3	2.9E-04	Multicopy suppressor of sec1; adjacent to Ty element YNRWsigma4		
0	0	TYE7	1.0	1.0E+00	3.9	4.6E-04	Basic helix-loop-helix transcription factor		
0	0	YNR051C	1.8	1.4E-02	3.8	4.7E-04	Similar to chicken nucleolin; adjacent to Ty element YNRWsigma4		
0	0	YNR048W	1.9	9.2E-03	3.9	4.9E-04	Protein of unknown function; adjacent to Ty element YNRWsigma4		
0	0	YGL050W	1.7	2.0E-02	3.8	5.1E-04	Protein of unknown function; adjacent to Ty element YGLCsigma3		
0	0	YIL036W	1.1	5.5E-01	3.4	8.2E-04	Similar to Mei4p and to CREB proteins; adjacent to YIL037C		
0	0	YNR067C	2.0	1.3E-02	3.4	1.1E-03	Protein of unknown function		
0	0	SDL1	1.6	7.2E-02	3.3	1.2E-03	Serine dehydratase; adjacent to YIL169C		
0	0	YDR281C	1.2	4.2E-01	3.1	1.7E-03	Protein of unknown function; adjacent to Ty element YDRWsigma5		
0	0	YDR100W	1.1	3.6E-01	5.5	1.9E-03	Protein of unknown function; adjacent to Ty element YDRCdelta9		
0	0	YNL043C	1.1	5.7E-01	3.0	2.1E-03	Protein of unknown function; adjacent to Ty element YNLWsigma2		
0	0	YOL154W	1.0	7.3E-01	3.0	2.1E-03	Similar to Zinc metalloproteinases; adjacent to YOL155C		
0	0	YHB1	1.0	8.3E-01	2.9	2.7E-03	Flavohemoglobin of unknown function; adjacent to PHO81		
0	0	PAN3	1.8	6.5E-02	4.6	3.5E-03	Component of Pab1p-stimulated poly(A) ribonuclease		
0	0	CWP2	1.8	1.5E-02	2.8	3.6E-03	major constituent of the cell wall containing GPI-anchor		
0	0	YKL097C	1.8	1.5E-02	2.8	3.6E-03	Protein of unknown function; adjacent to CWP2		

FIGURE 7C

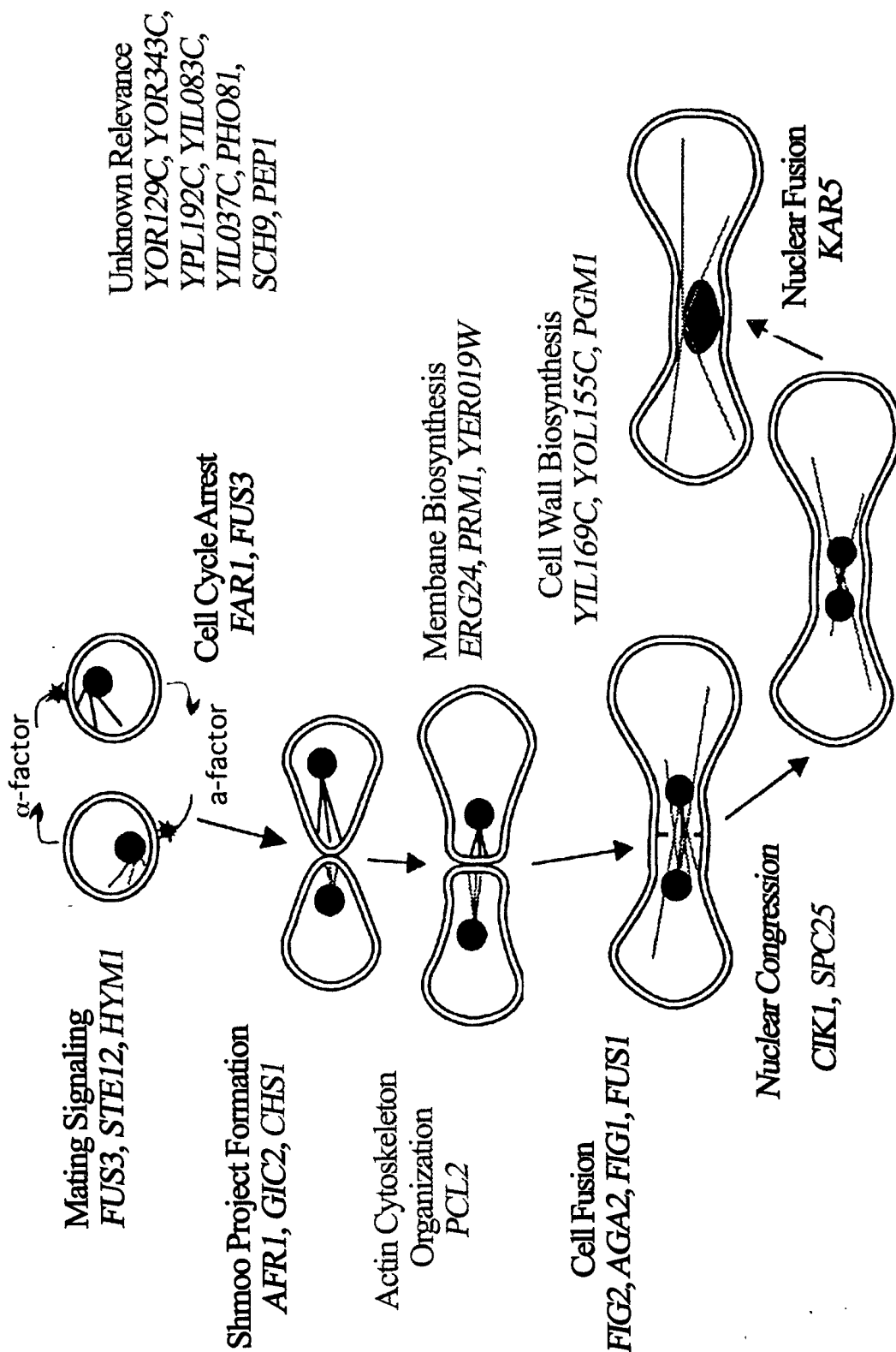


FIGURE 8

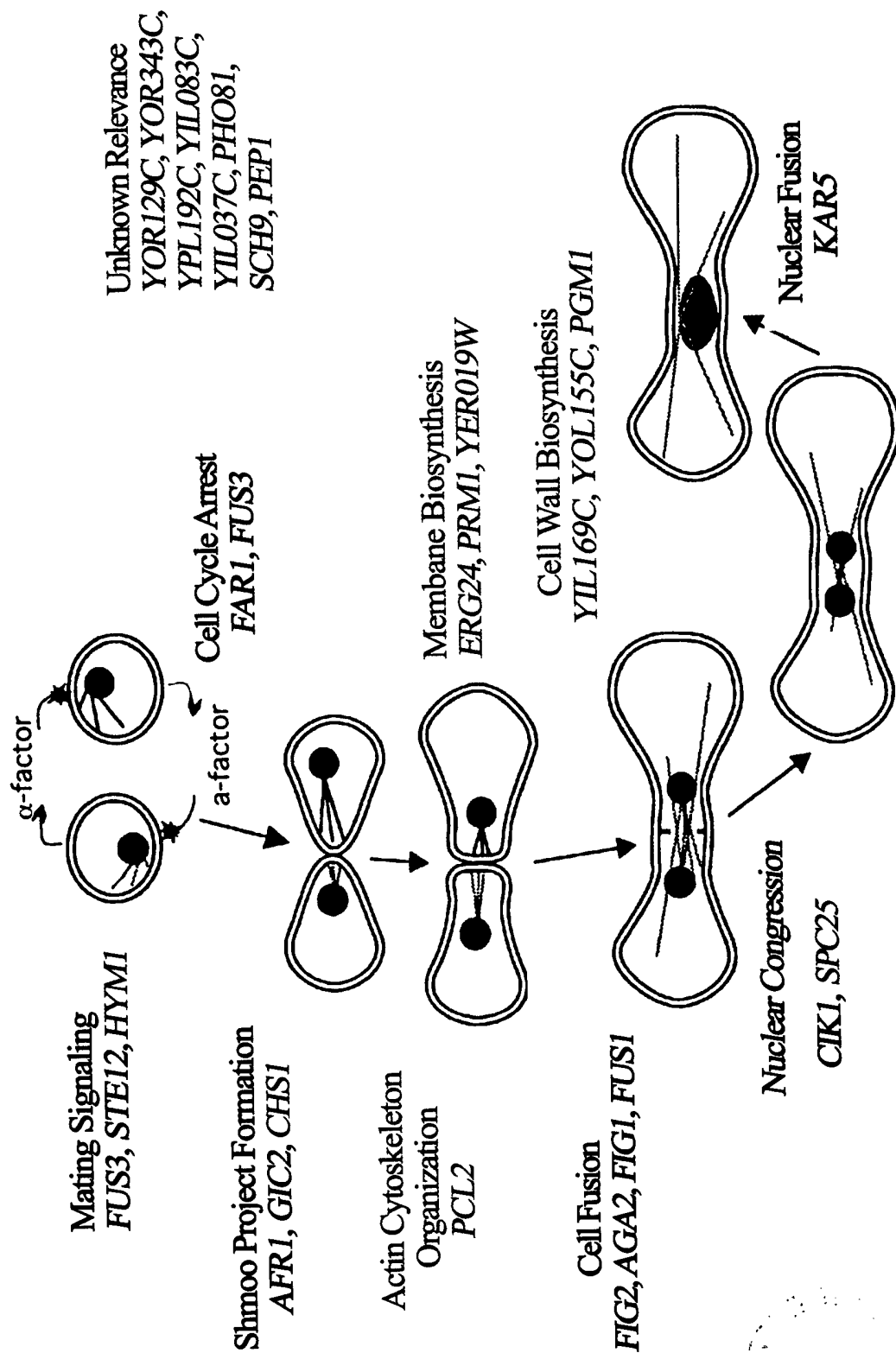


FIGURE 8

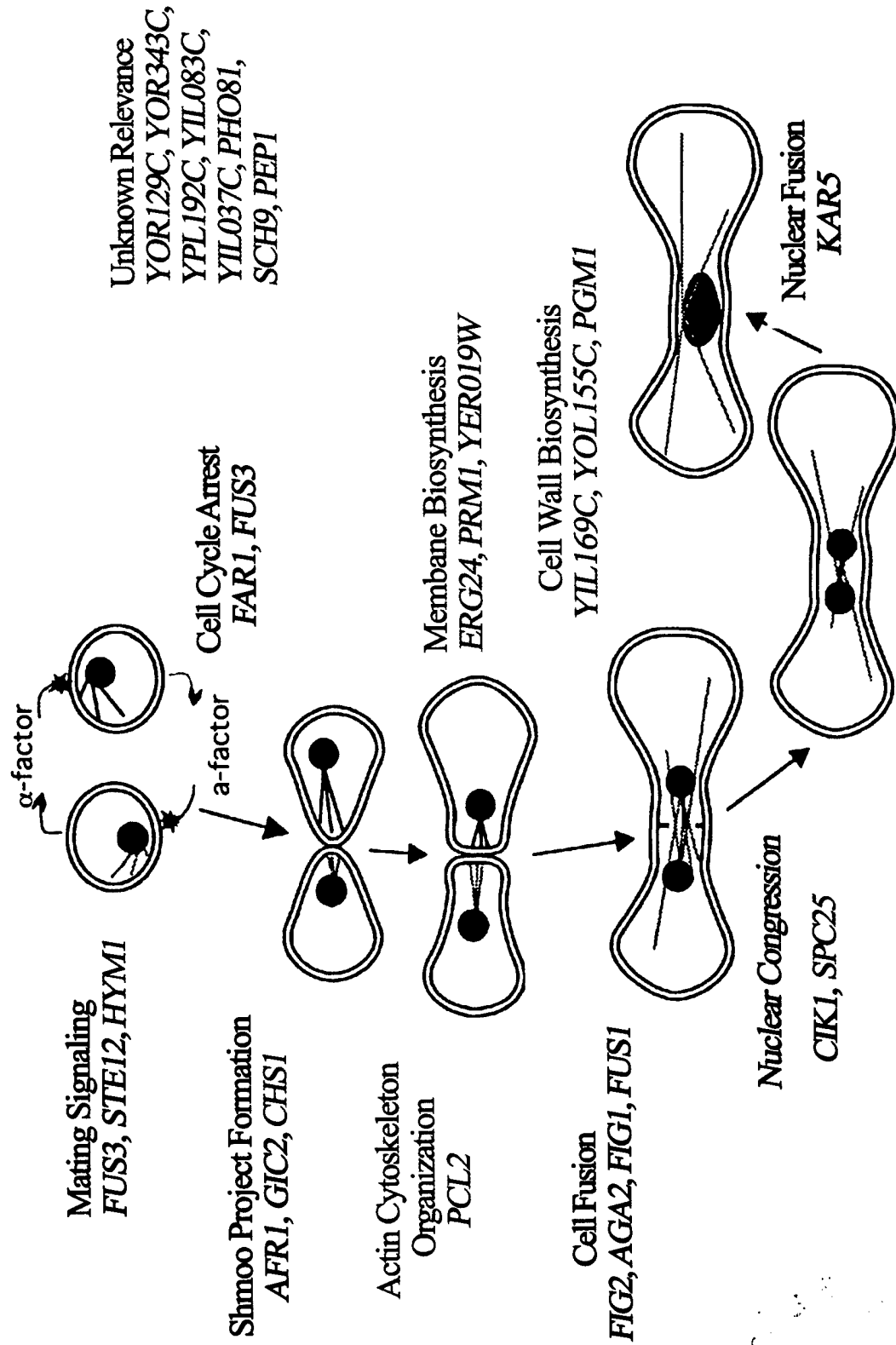


FIGURE 8

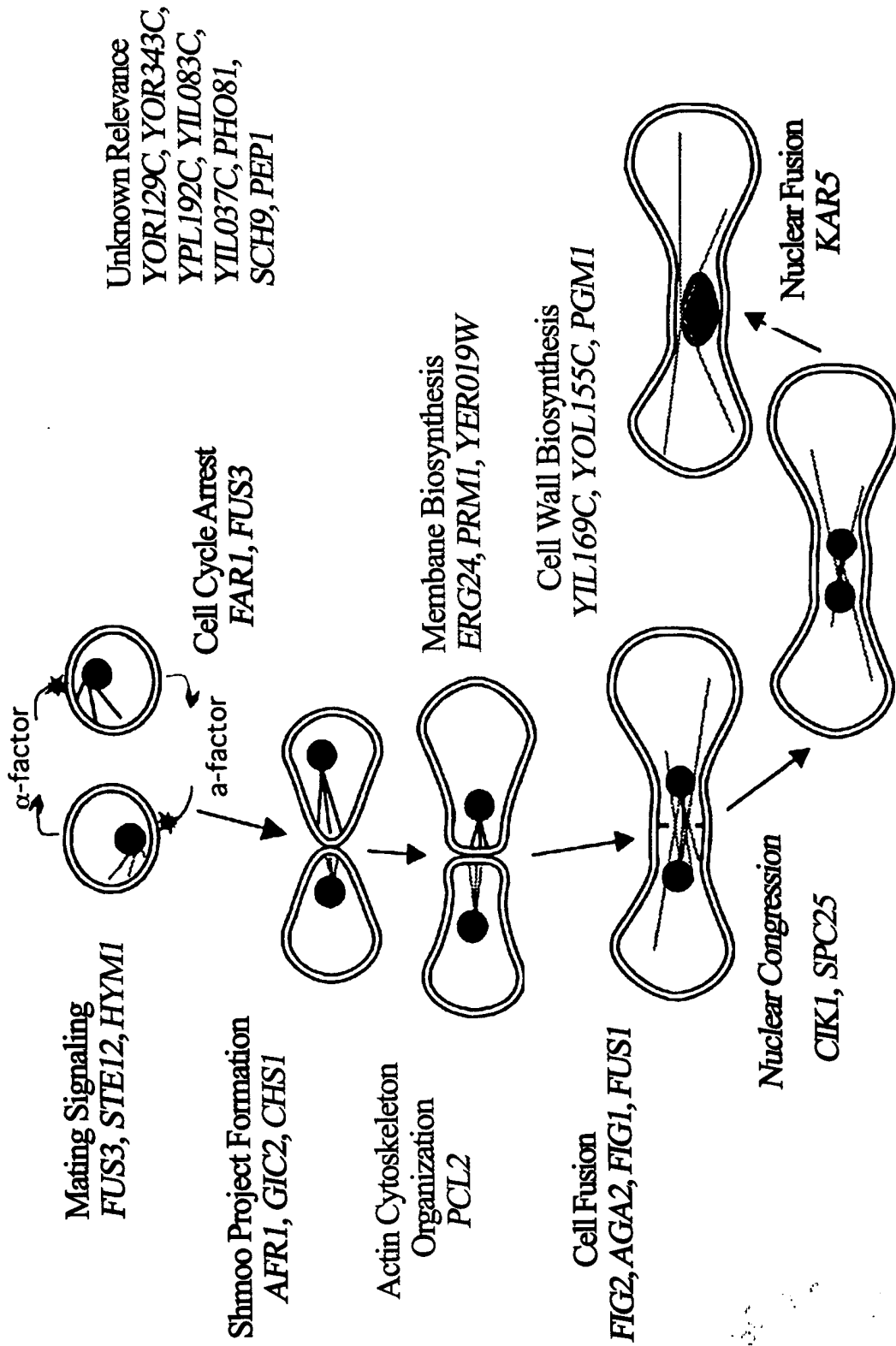


FIGURE 8

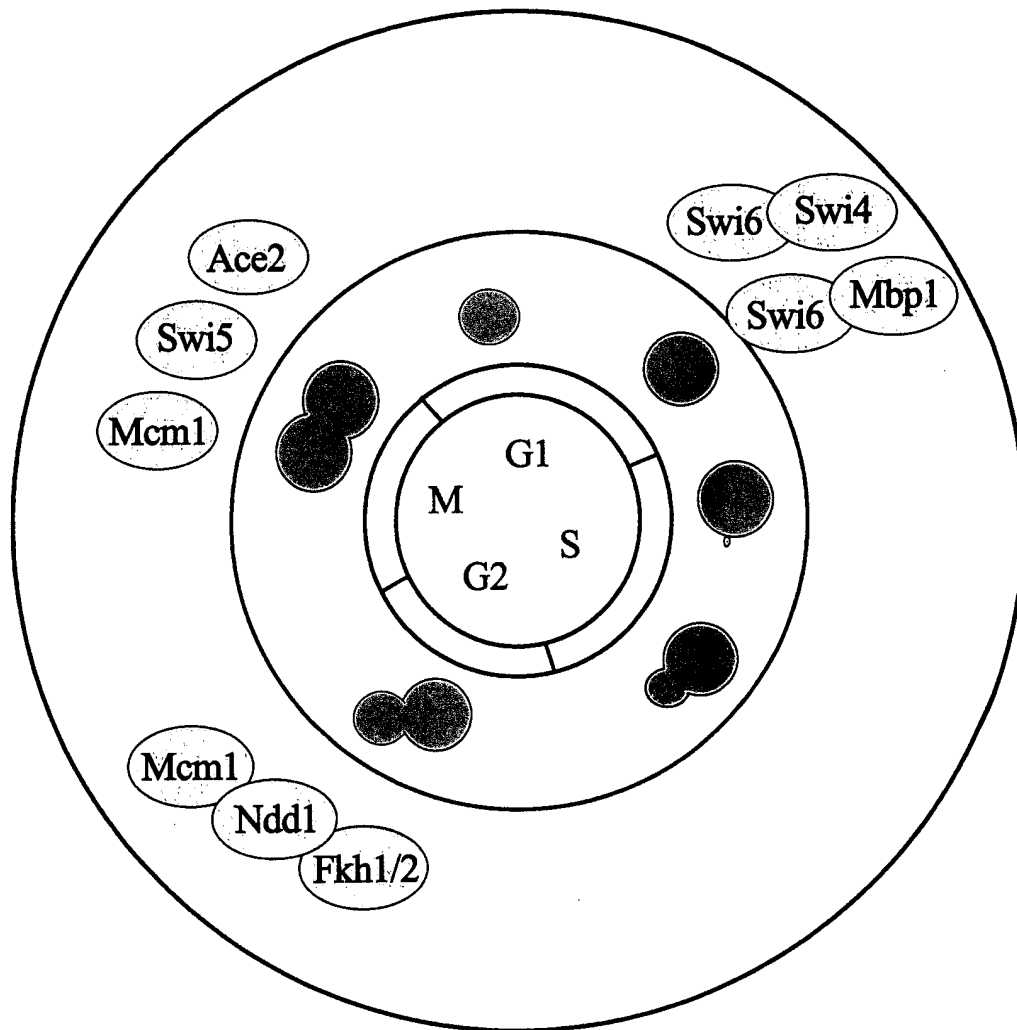


FIGURE 9A

[illegible]

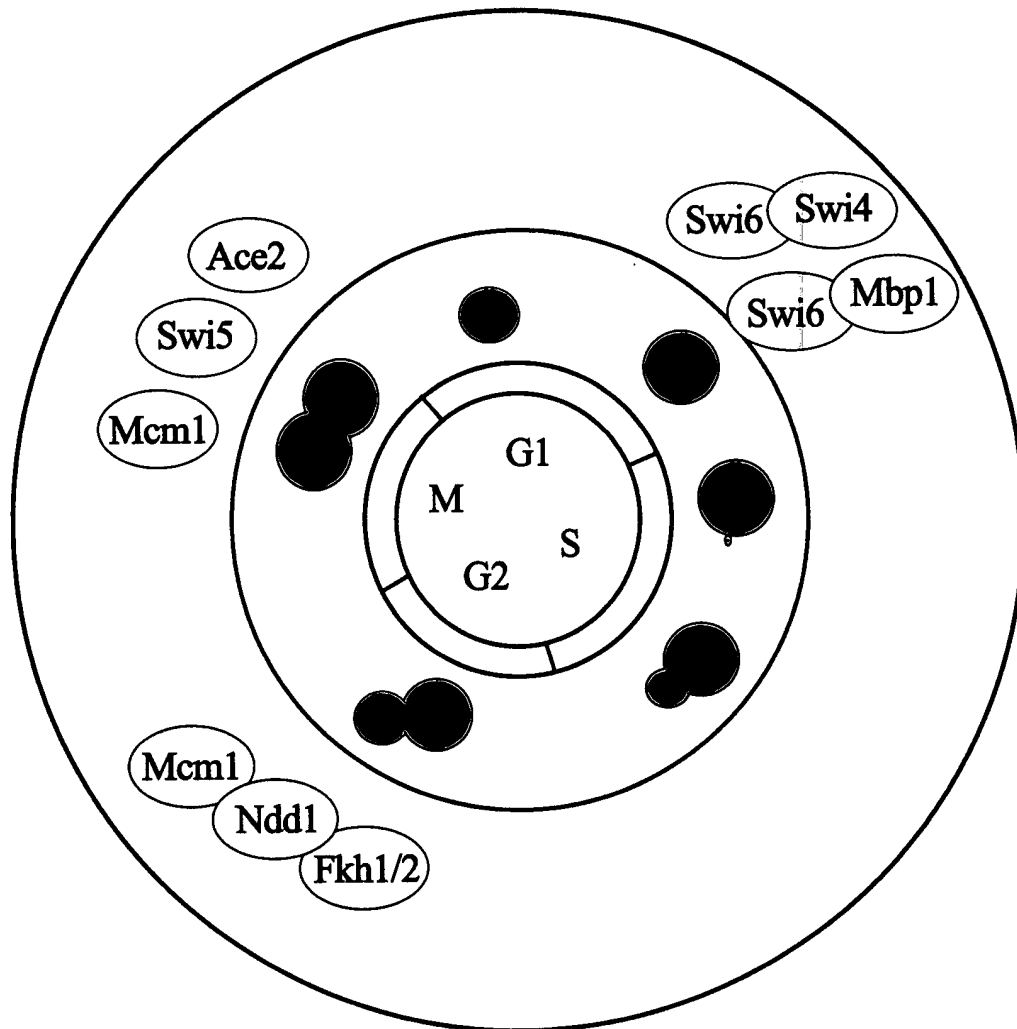


FIGURE 9A

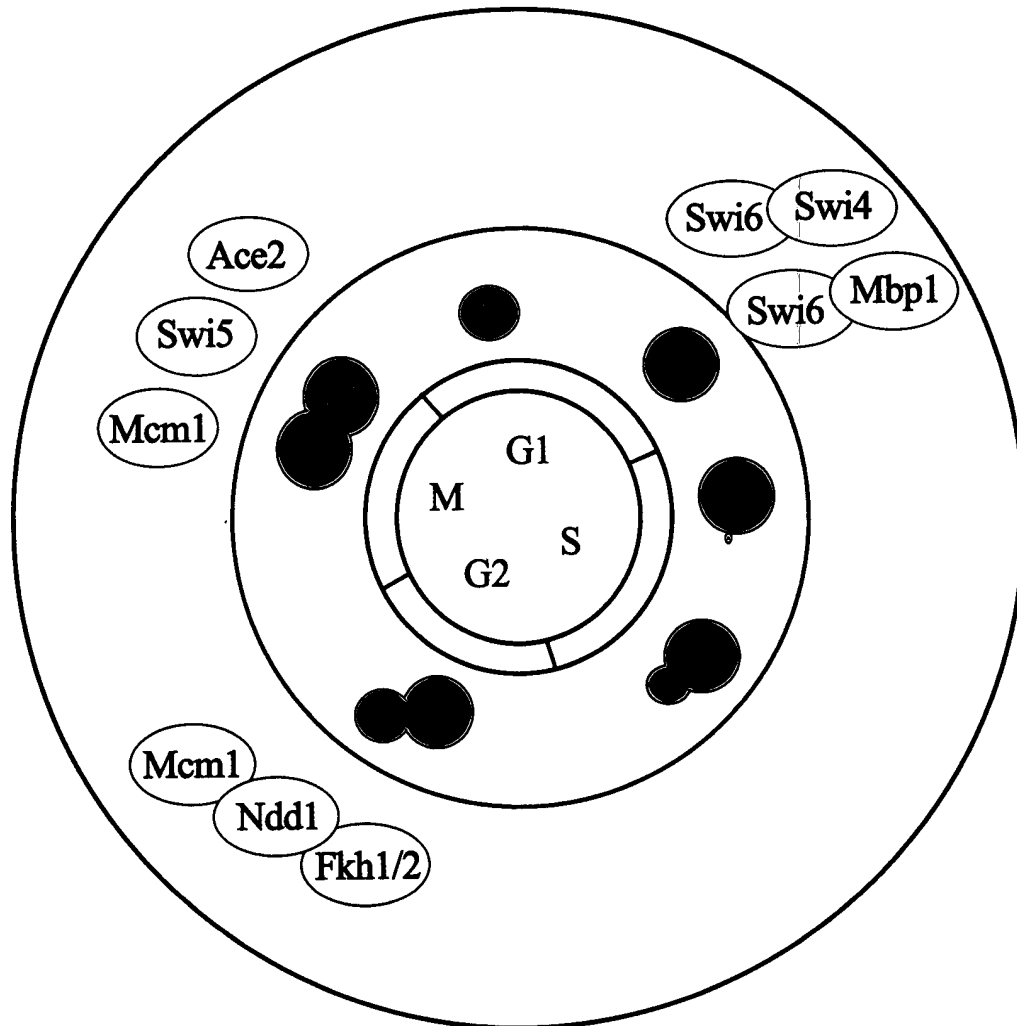


FIGURE 9A

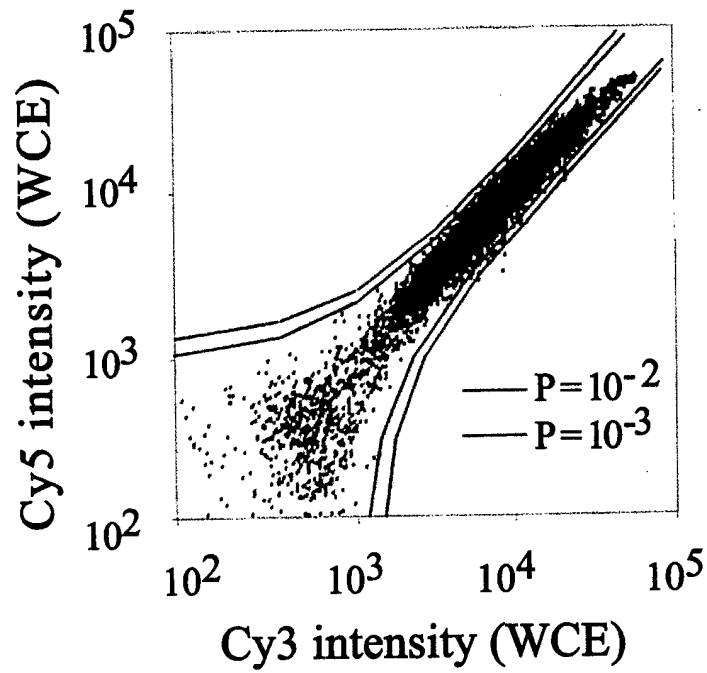


FIGURE 9B

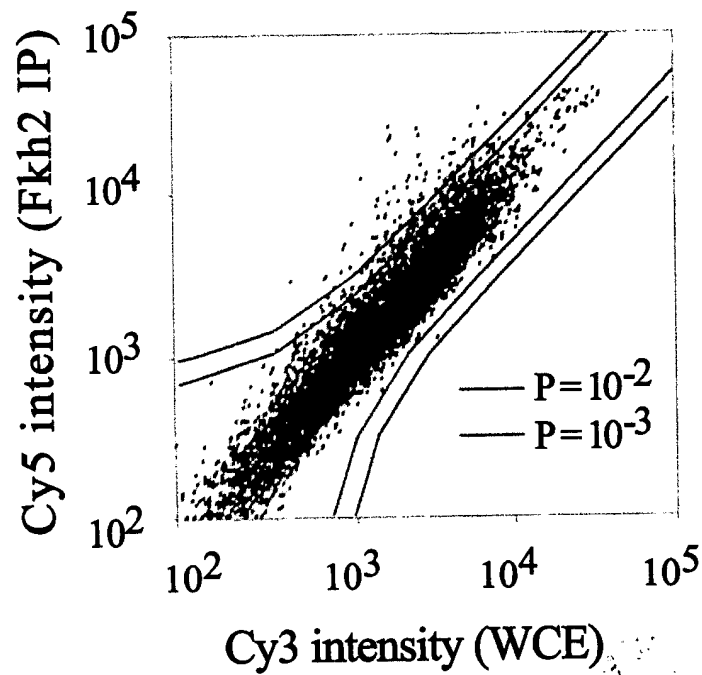


FIGURE 9C

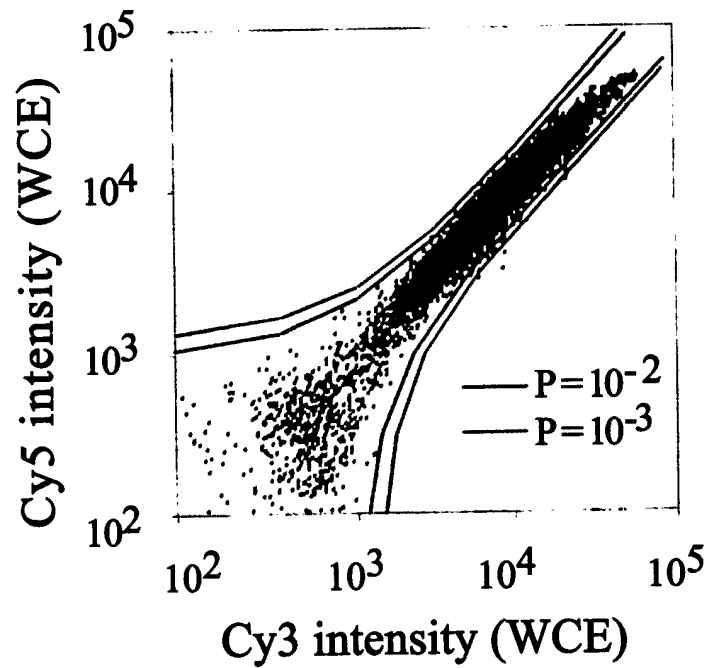


FIGURE 9B

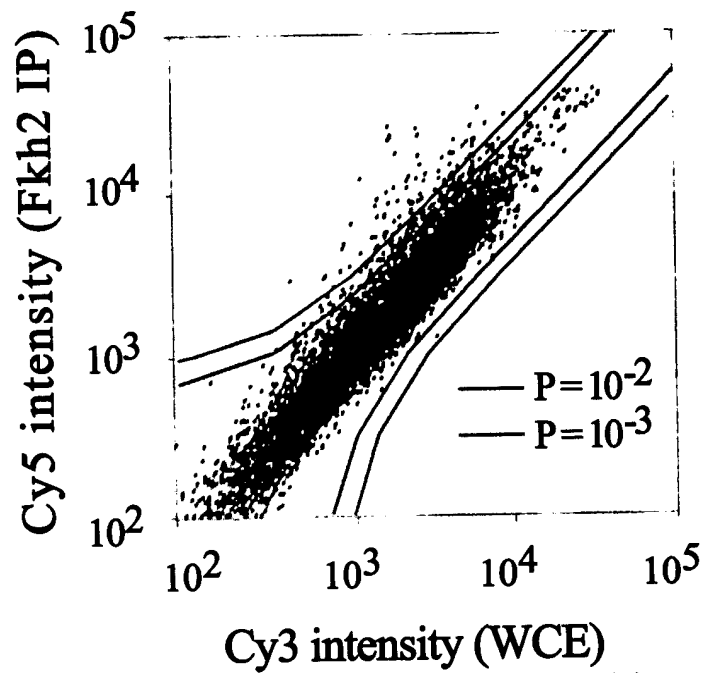


FIGURE 9C

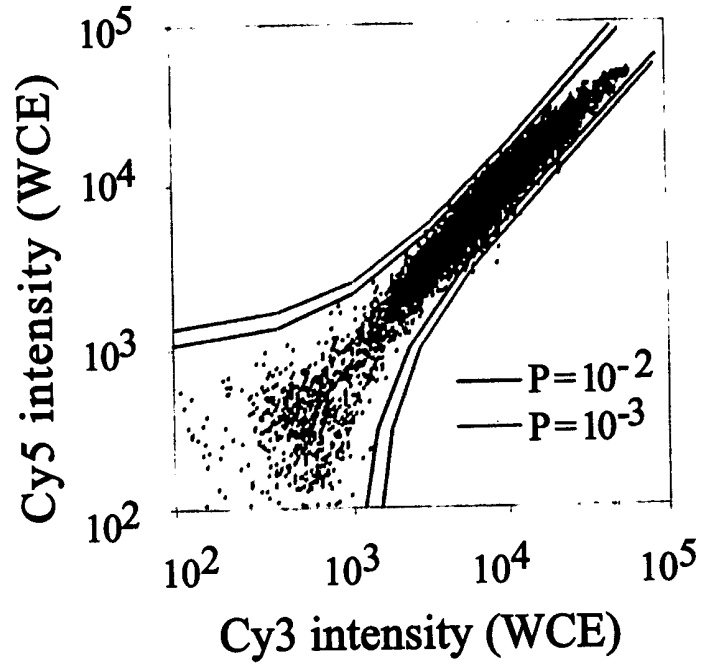


FIGURE 9B

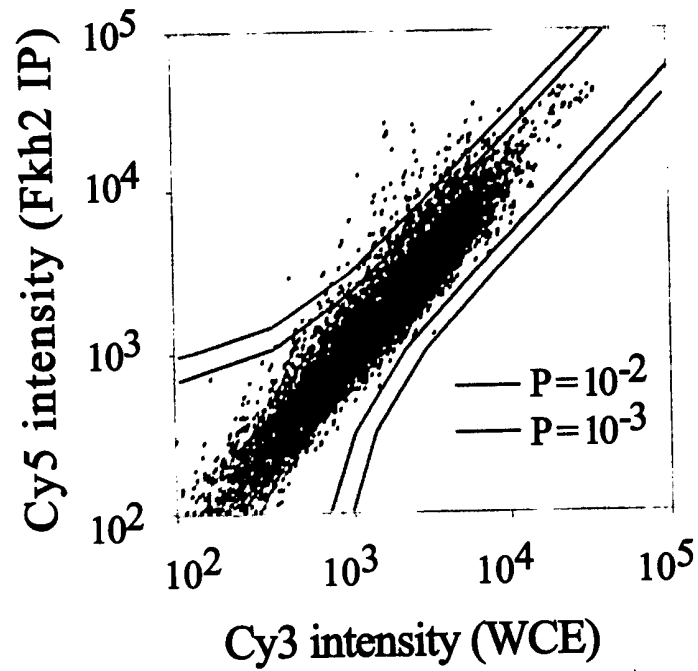


FIGURE 9C

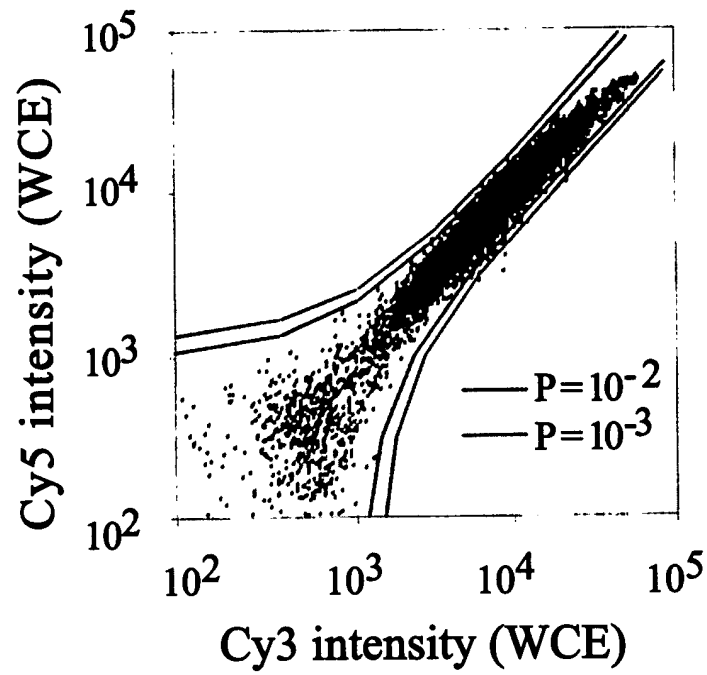


FIGURE 9B

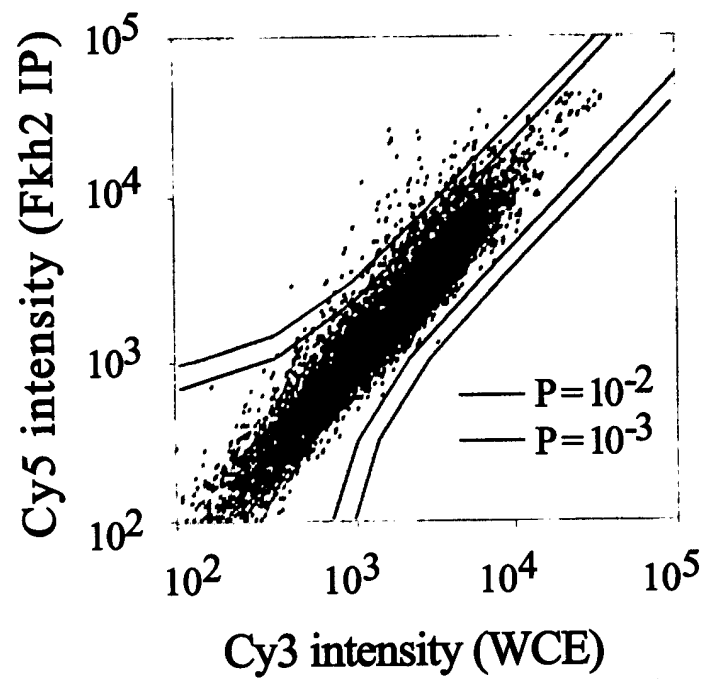


FIGURE 9C

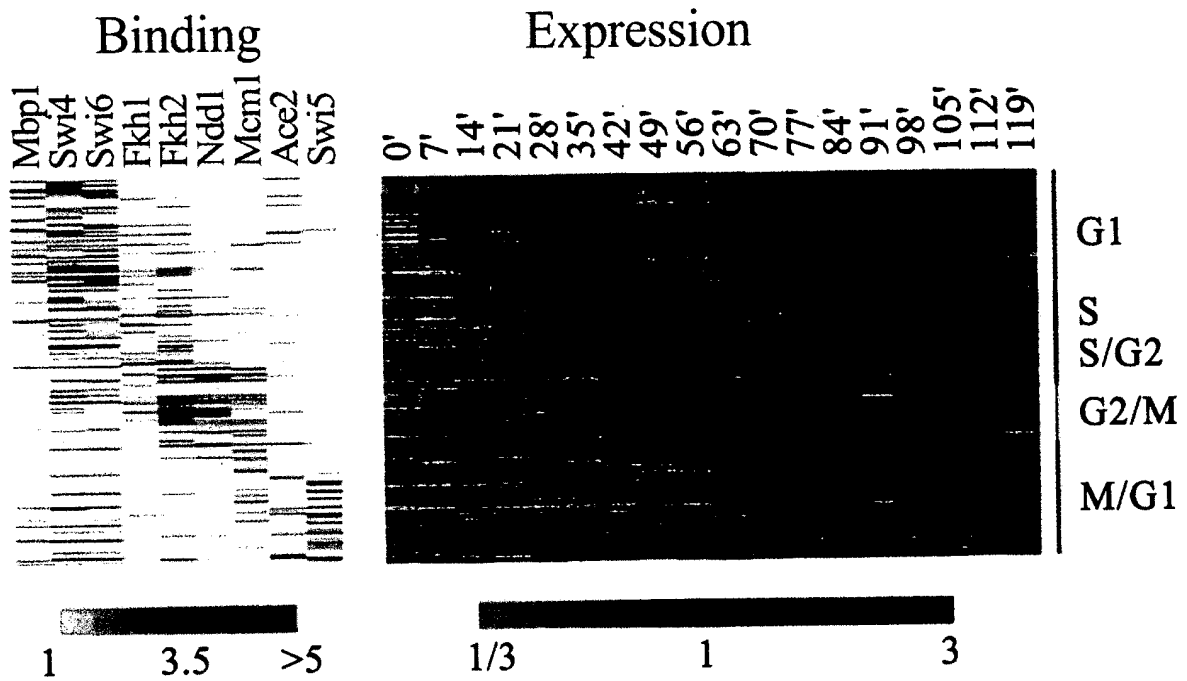


FIGURE 10A

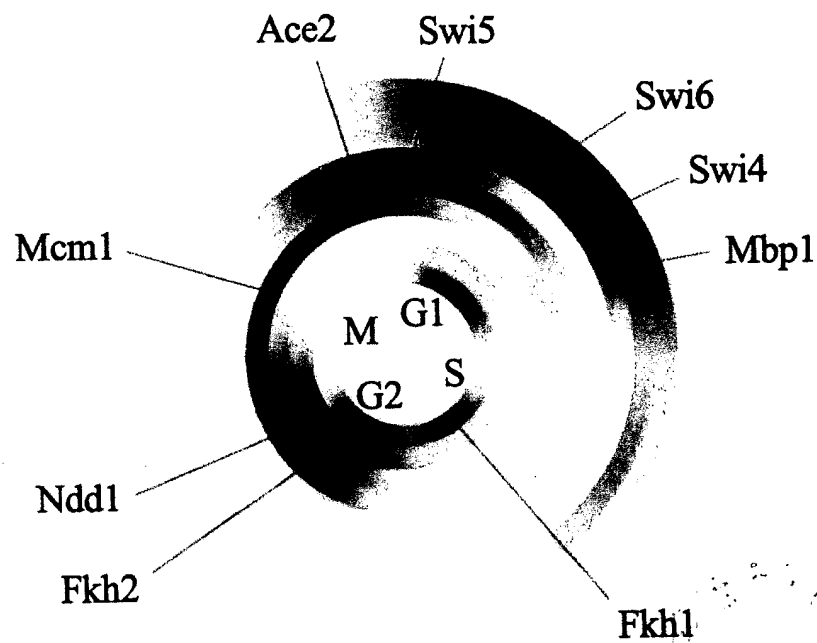


FIGURE 10B

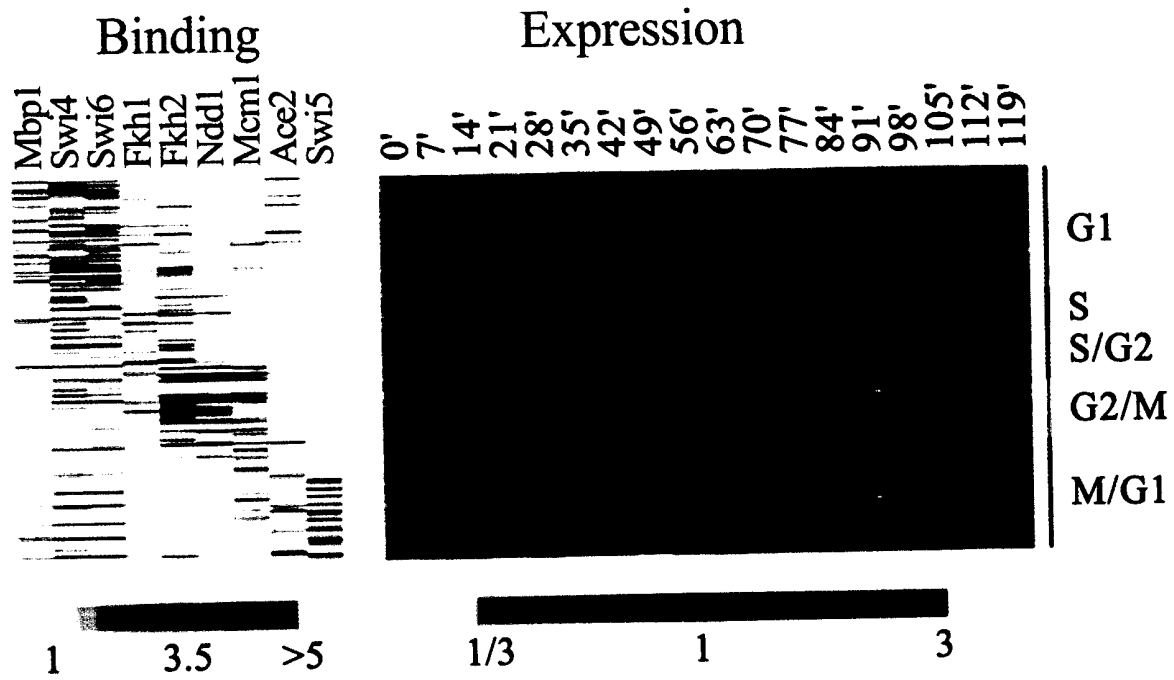


FIGURE 10A

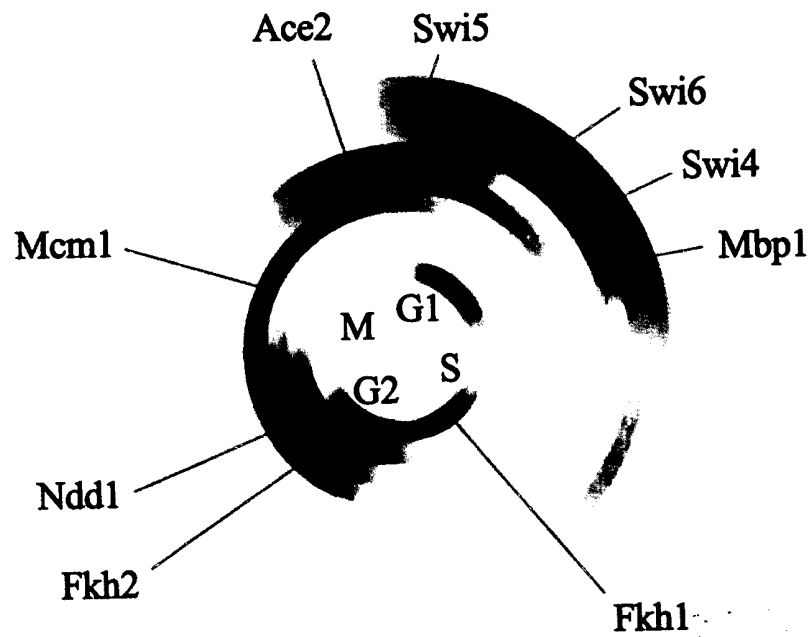


FIGURE 10B

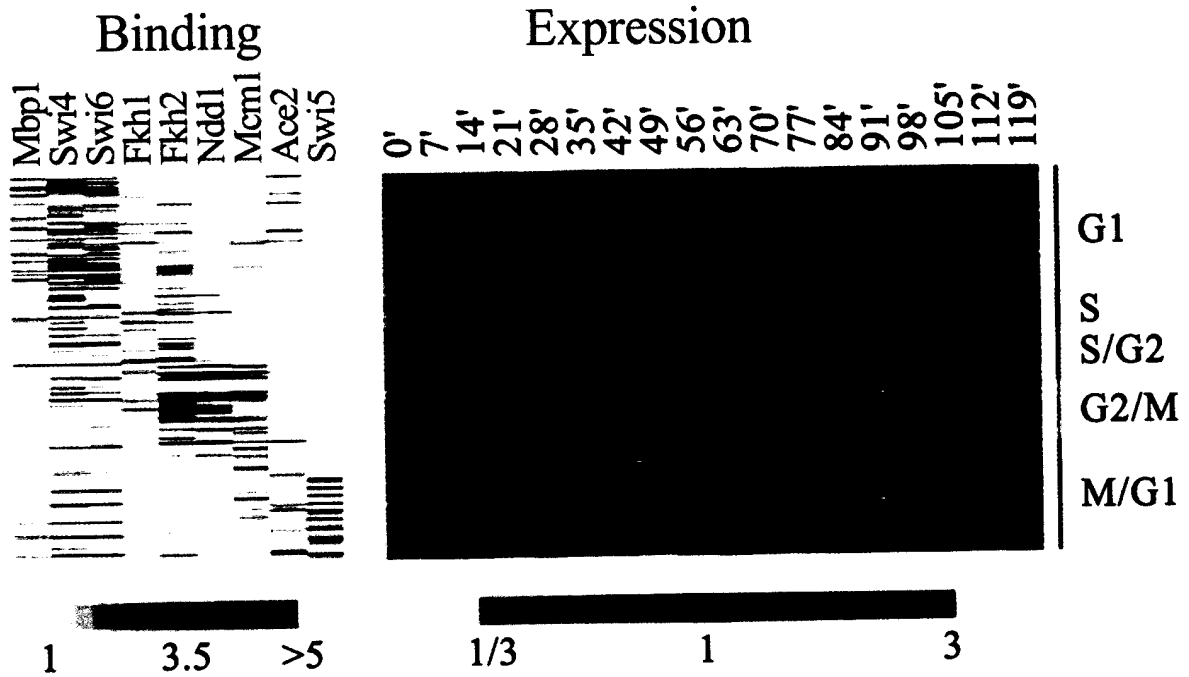


FIGURE 10A

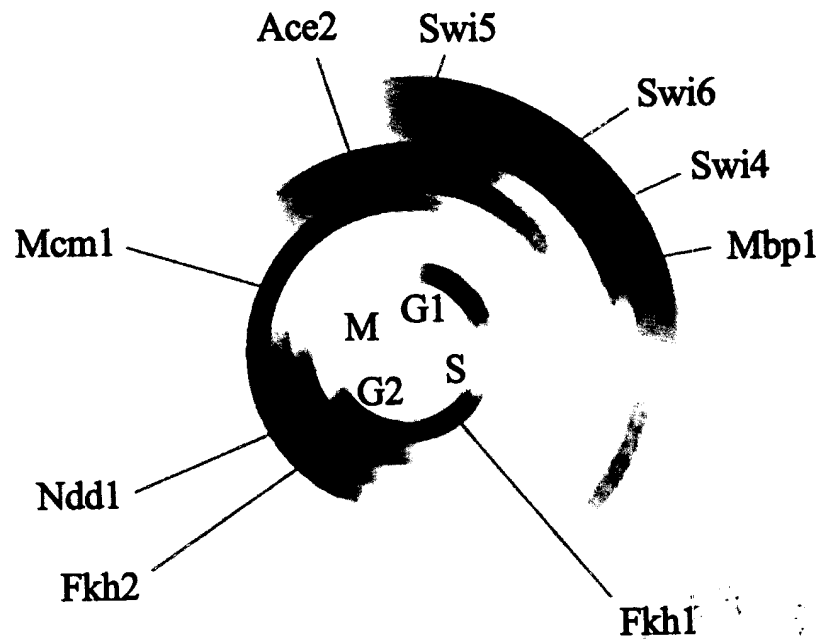


FIGURE 10B

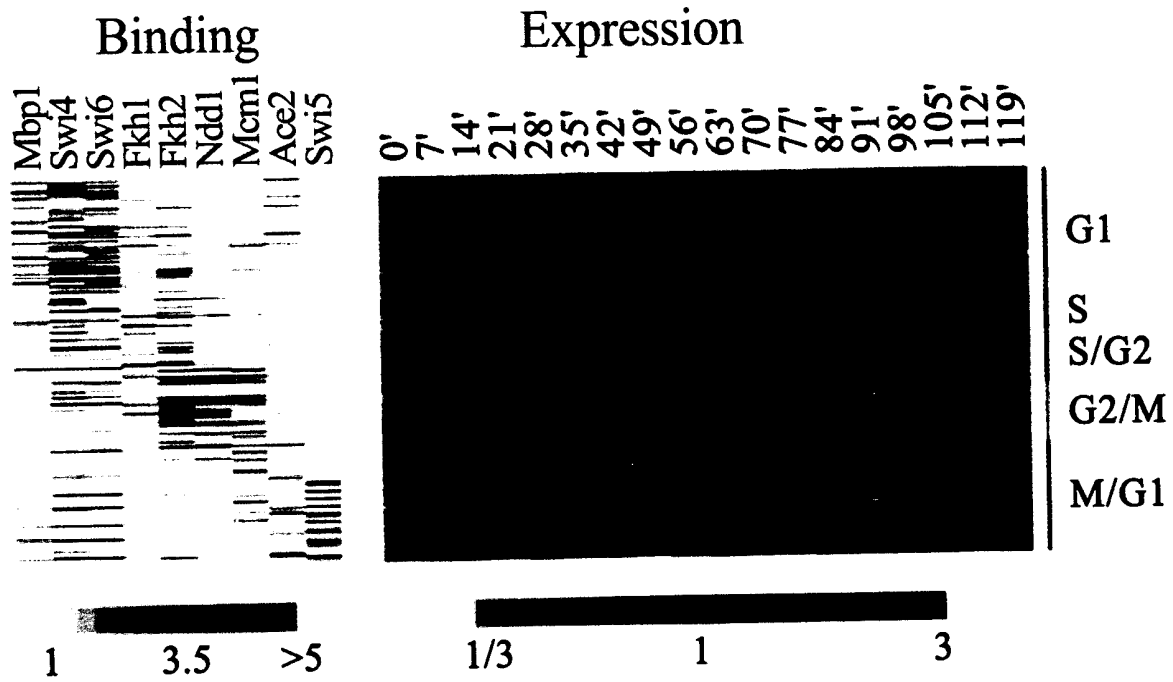


FIGURE 10A

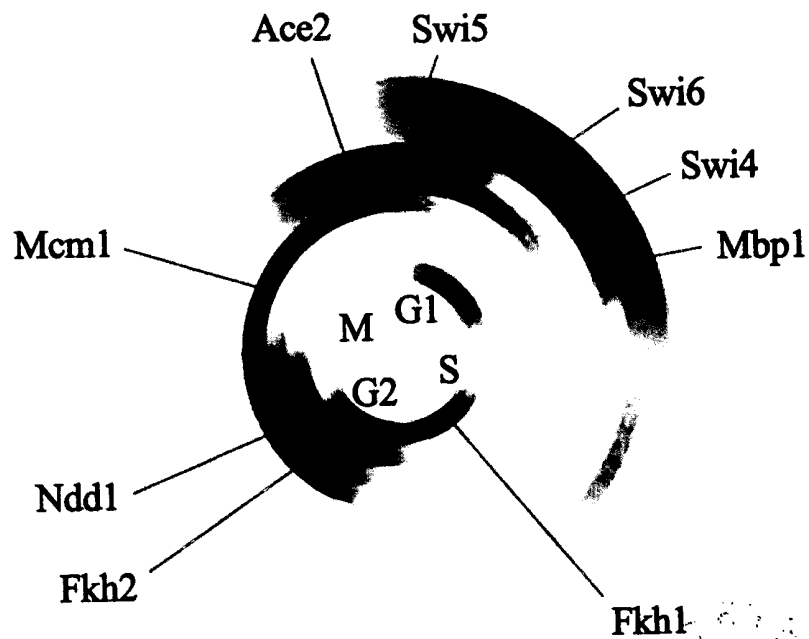


FIGURE 10B

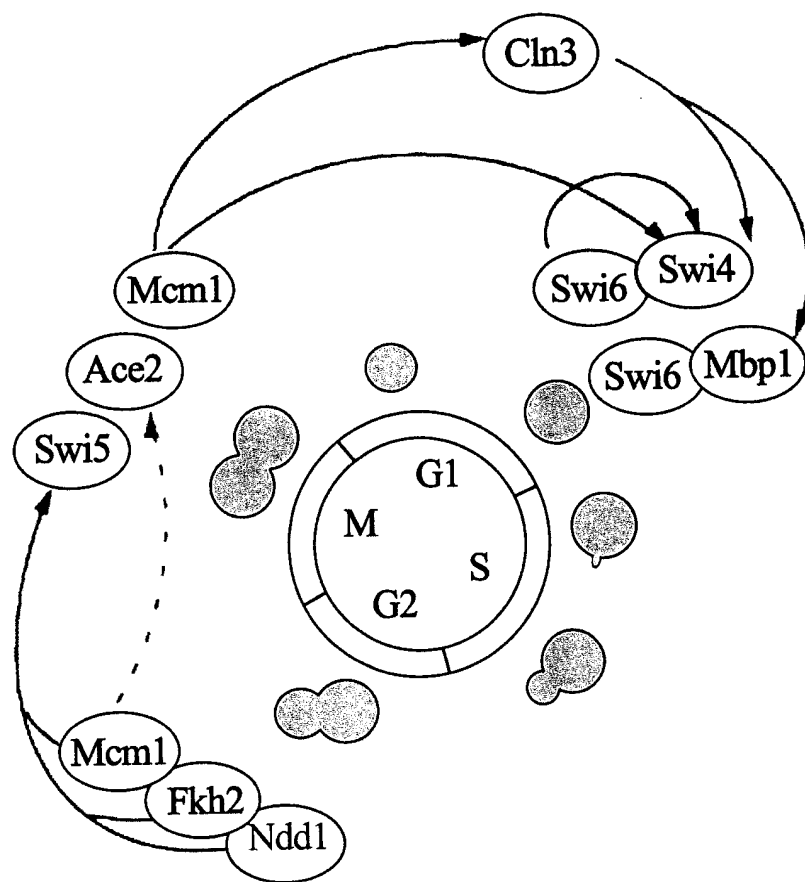


FIGURE 11A

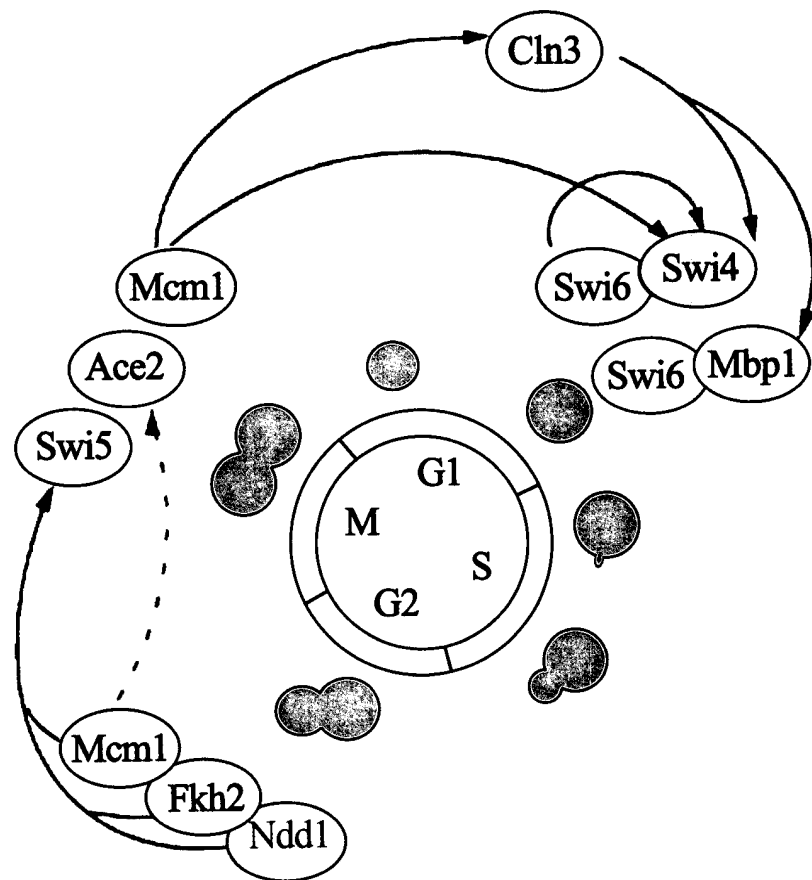


FIGURE 11A

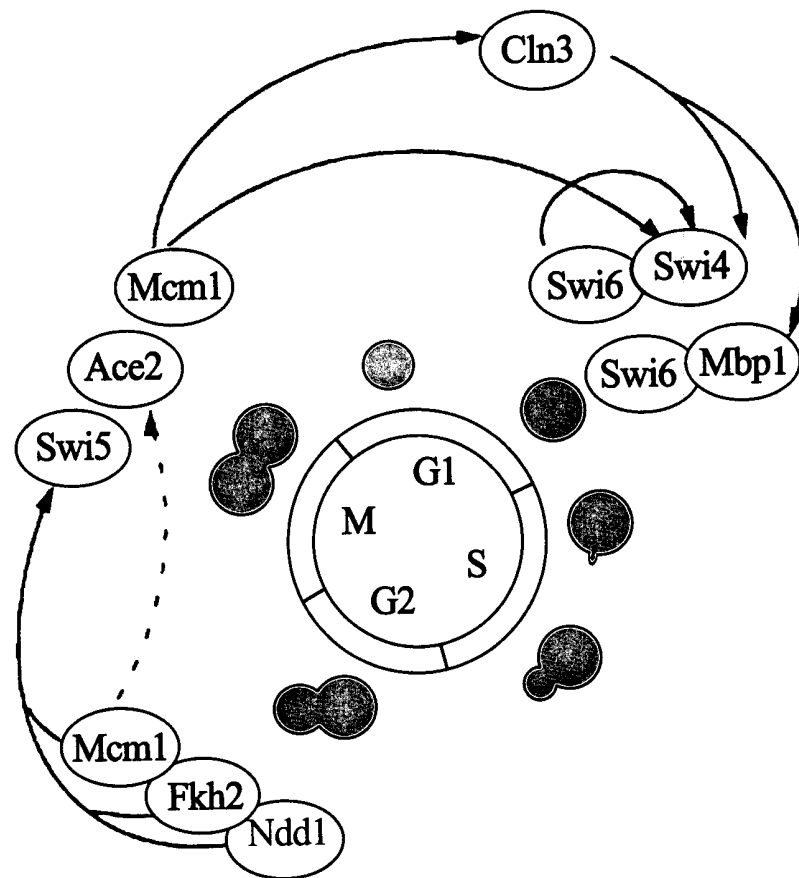


FIGURE 11A

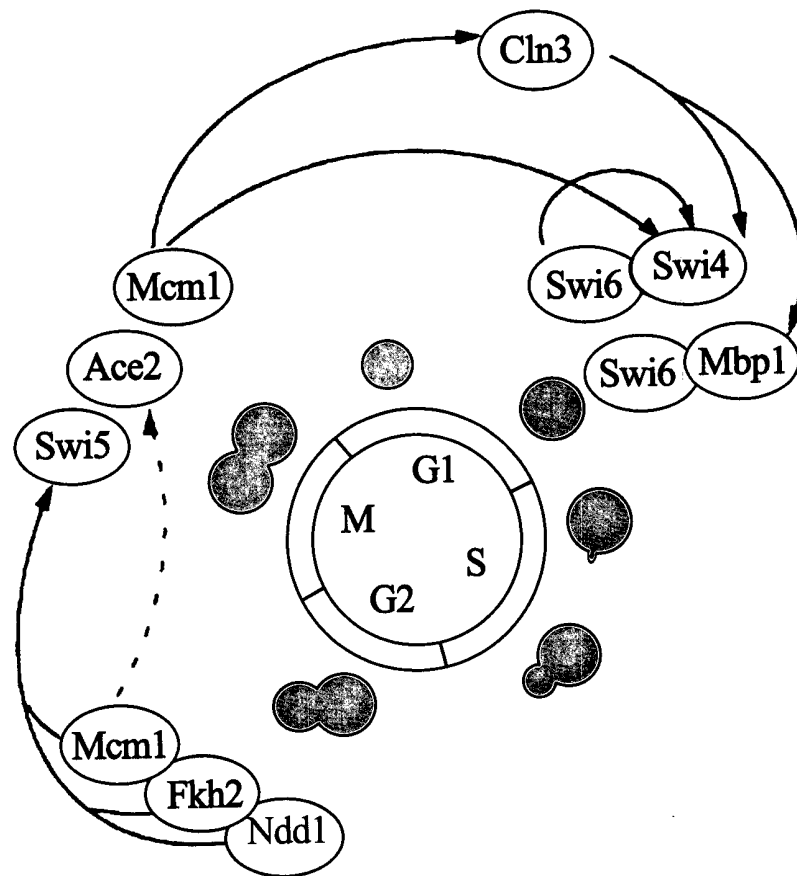


FIGURE 11A

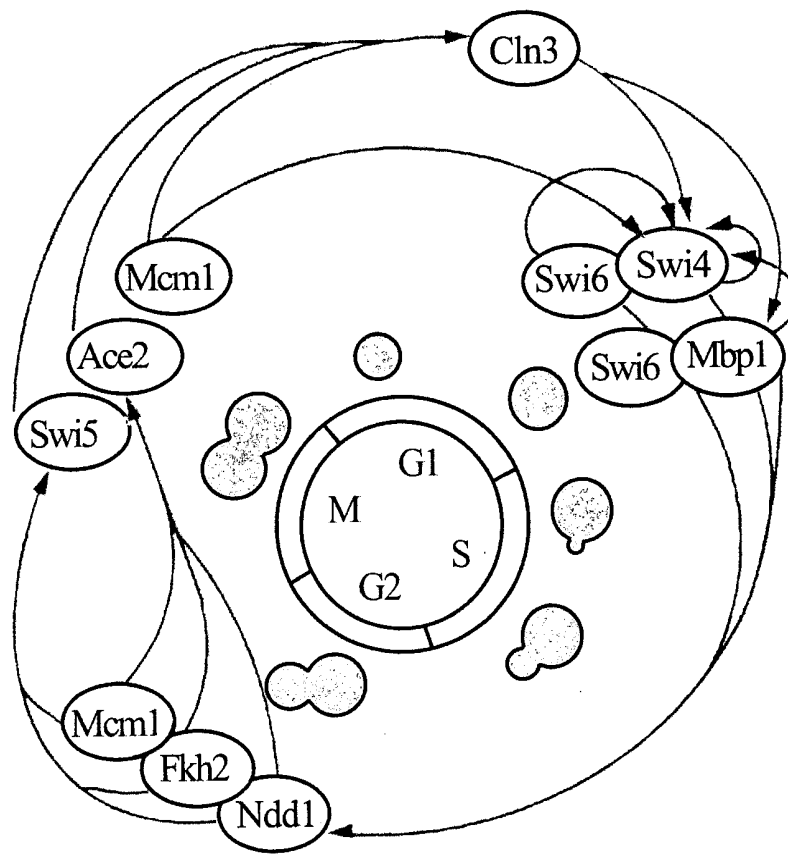


FIGURE 11B

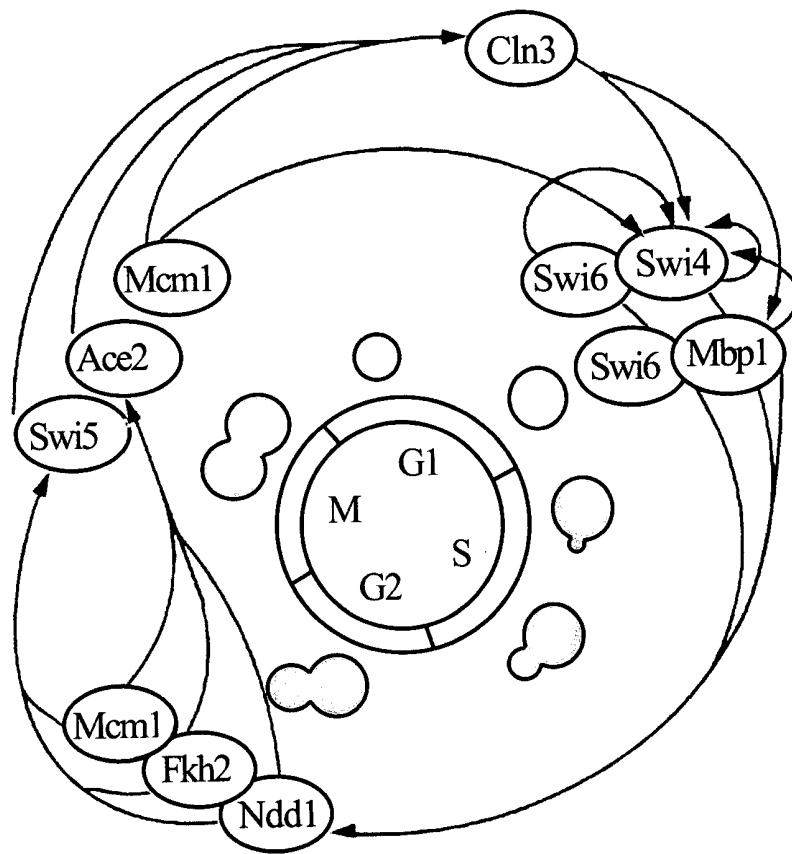


FIGURE 11B

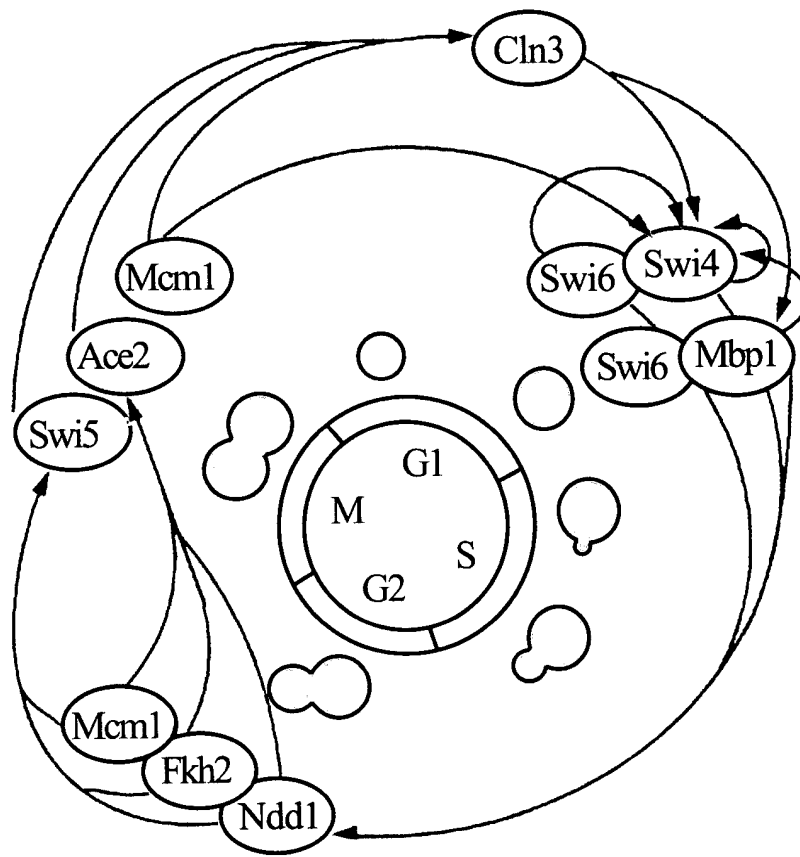


FIGURE 11B

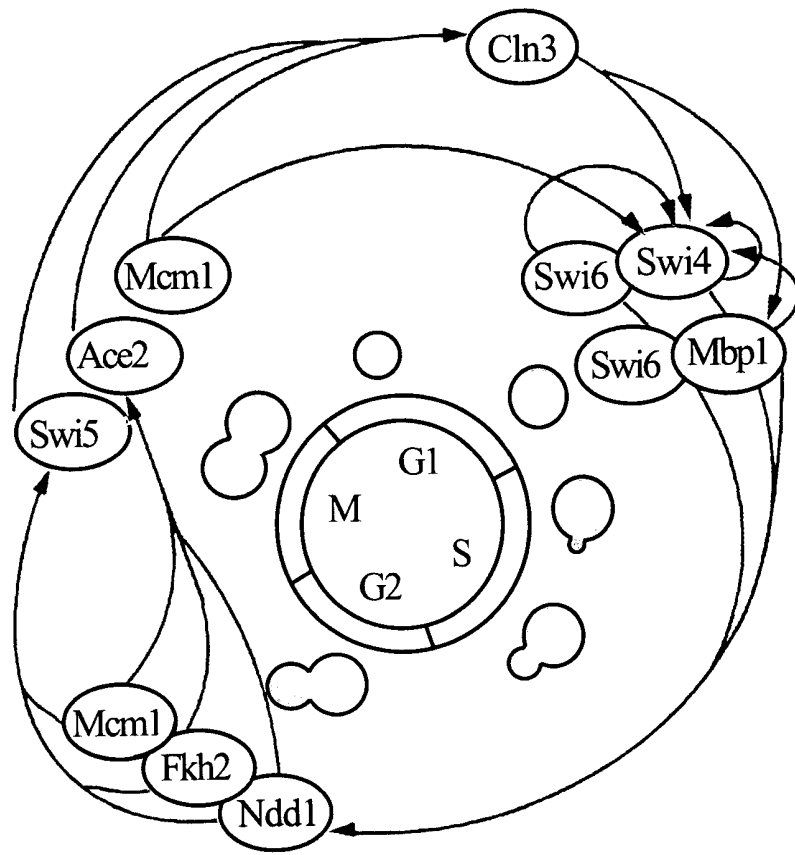


FIGURE 11B

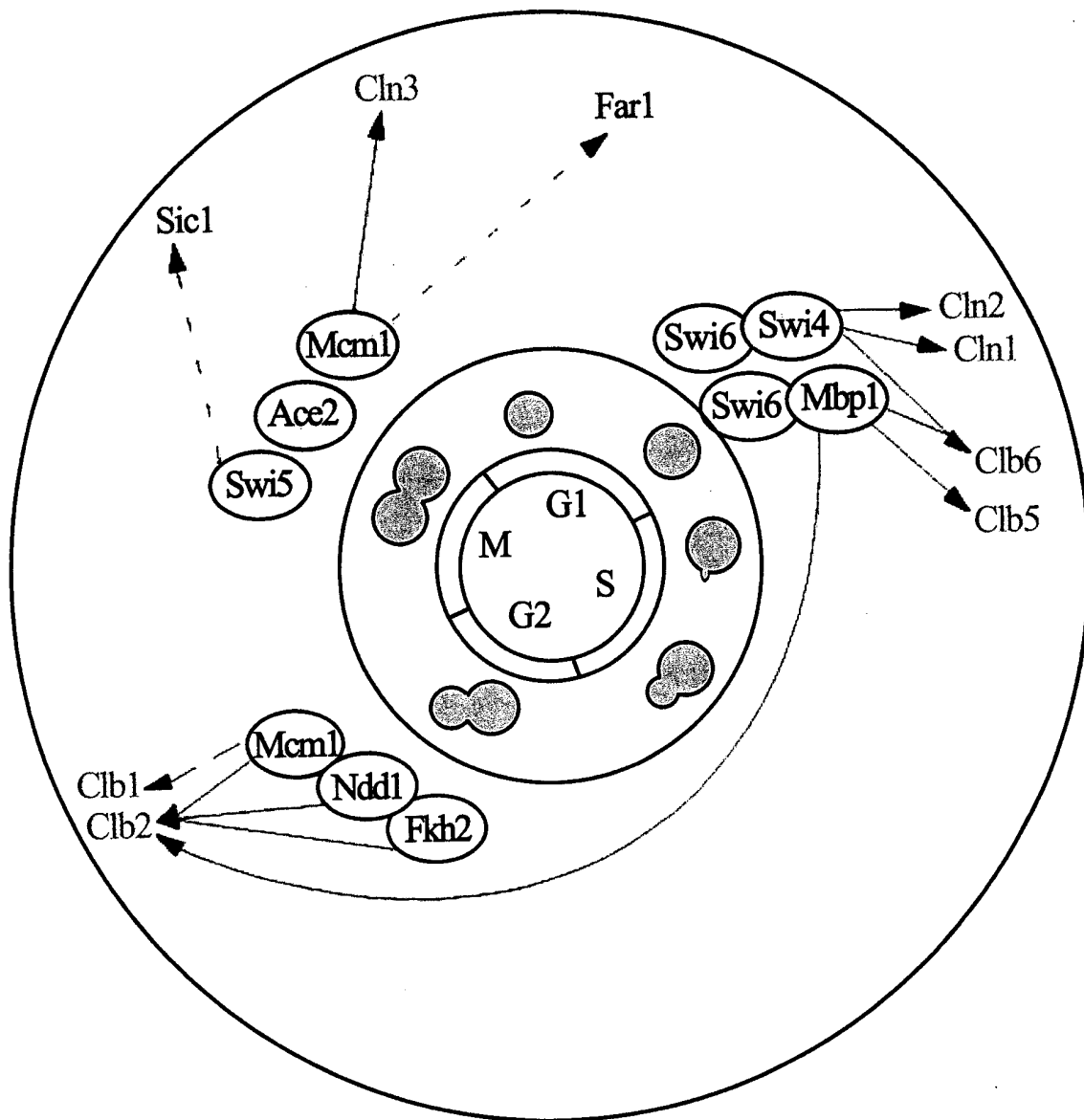


FIGURE 12A

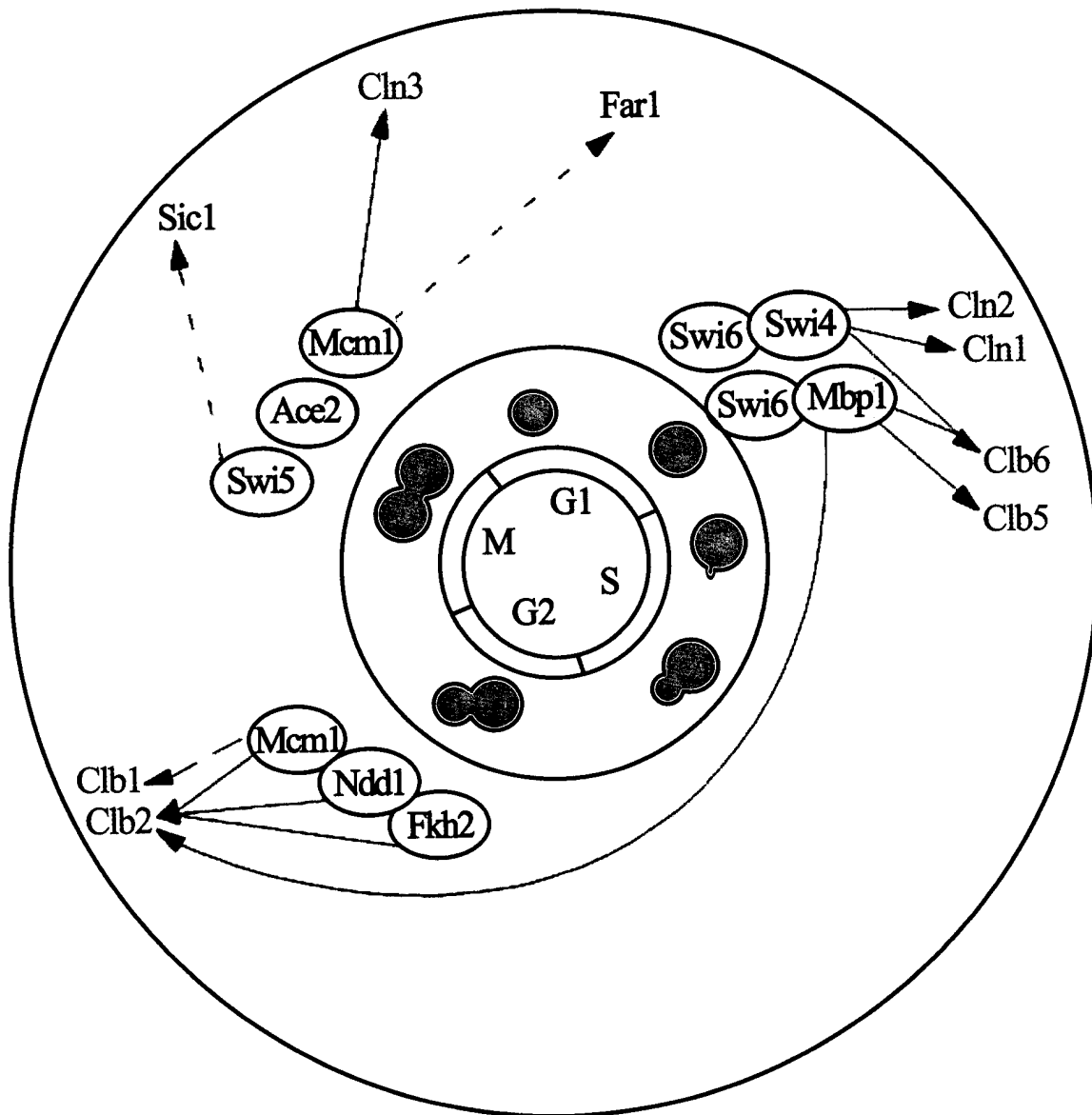


FIGURE 12A

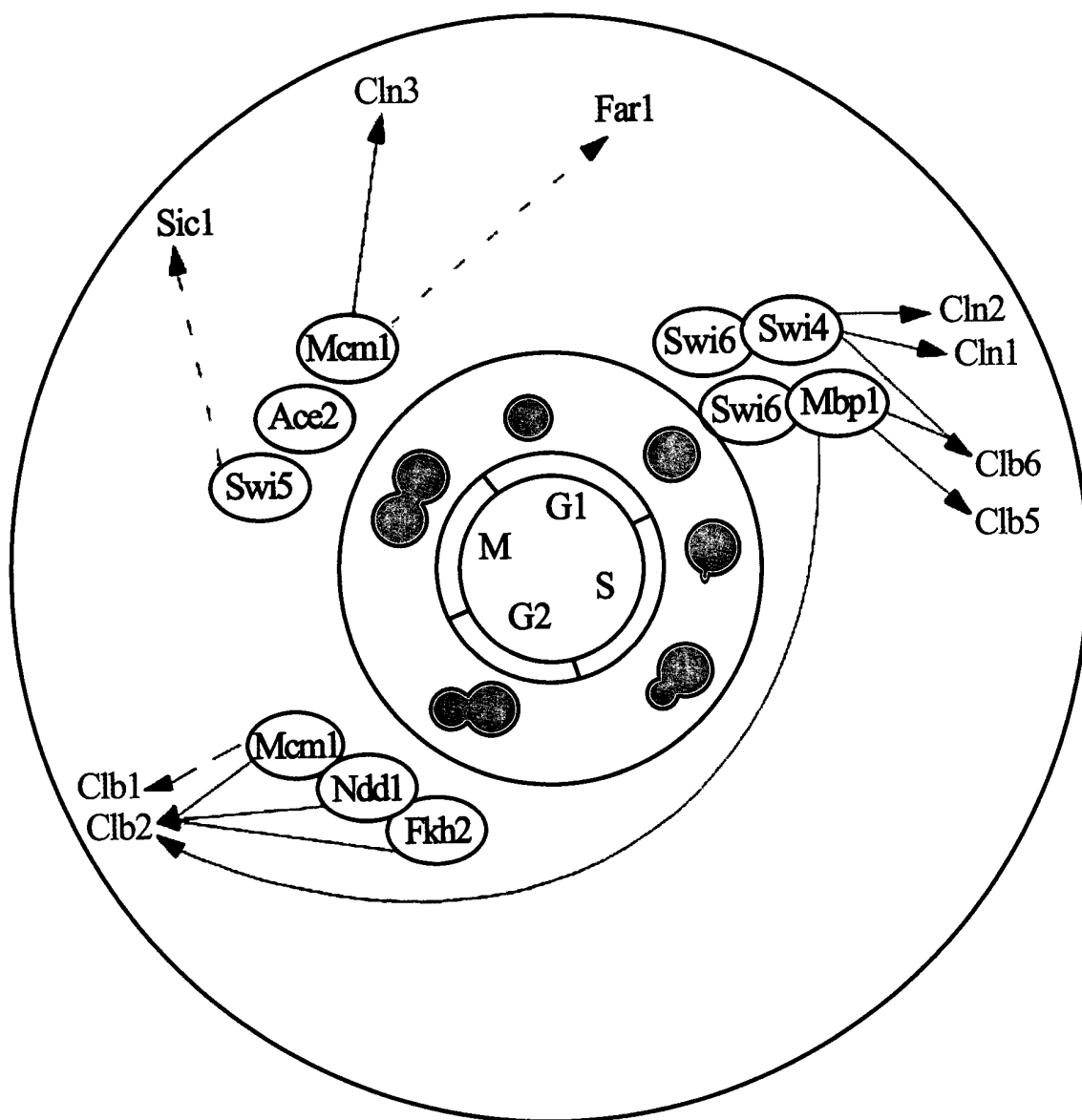


FIGURE 12A

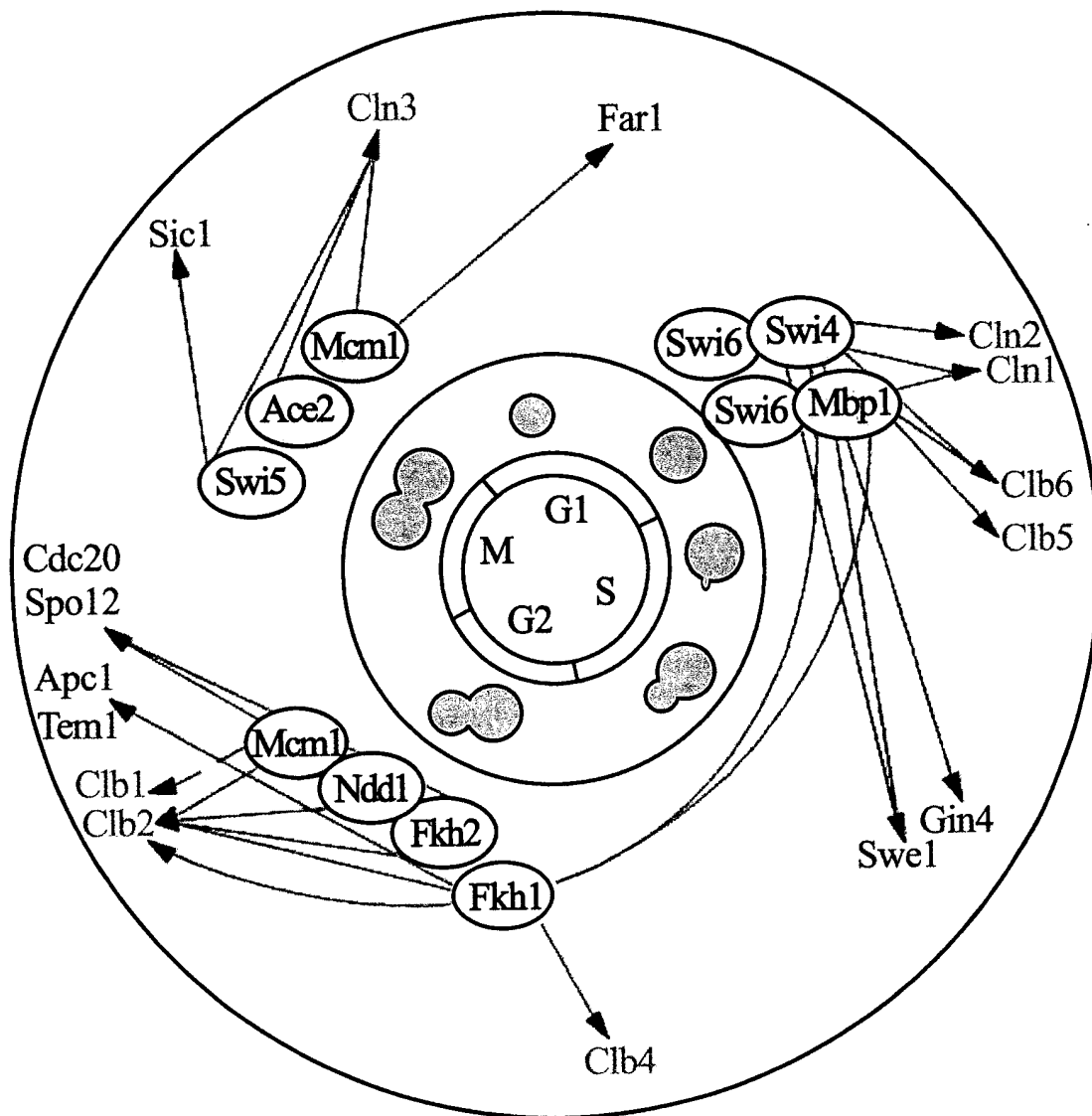


FIGURE 12B

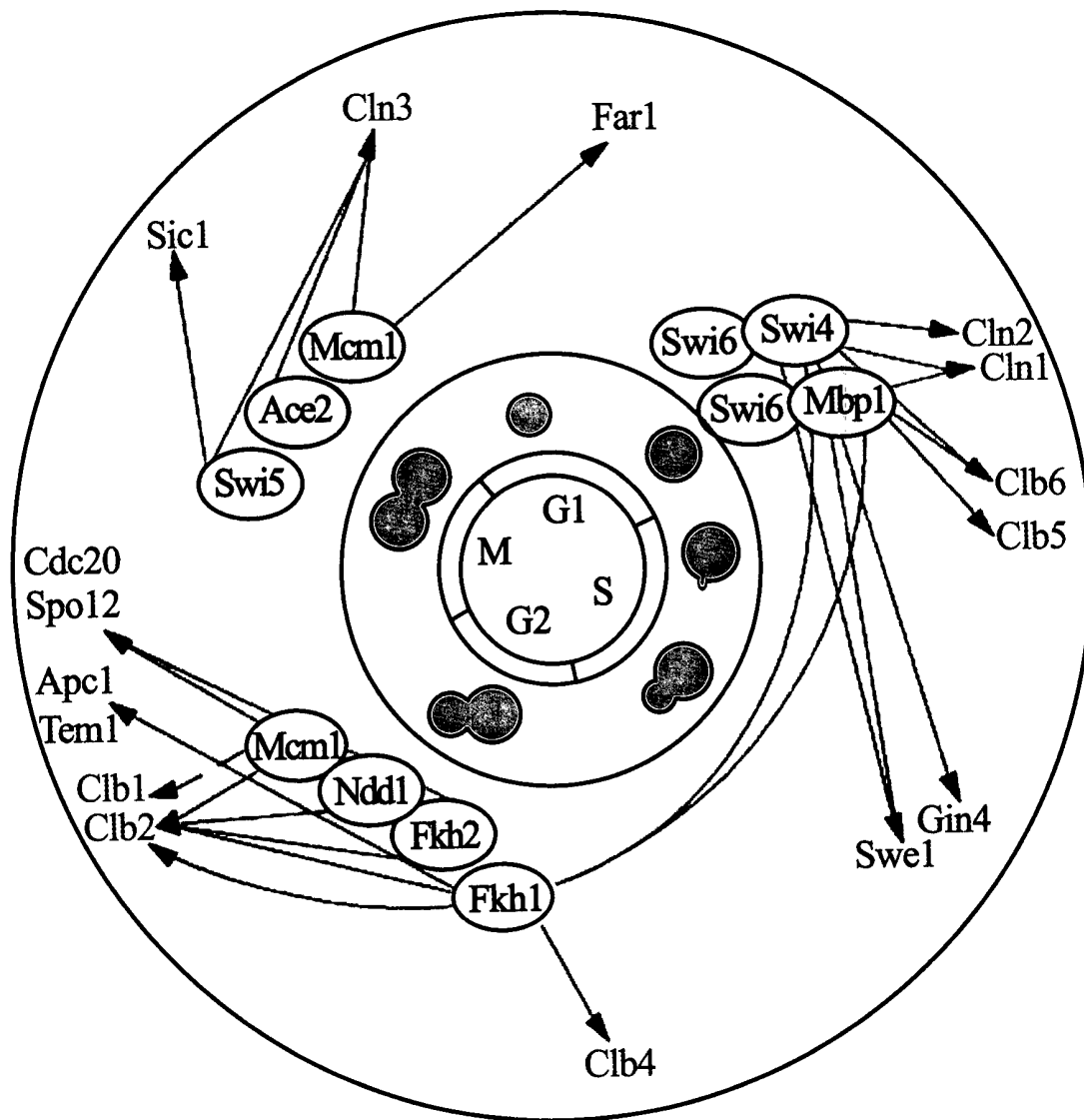


FIGURE 12B

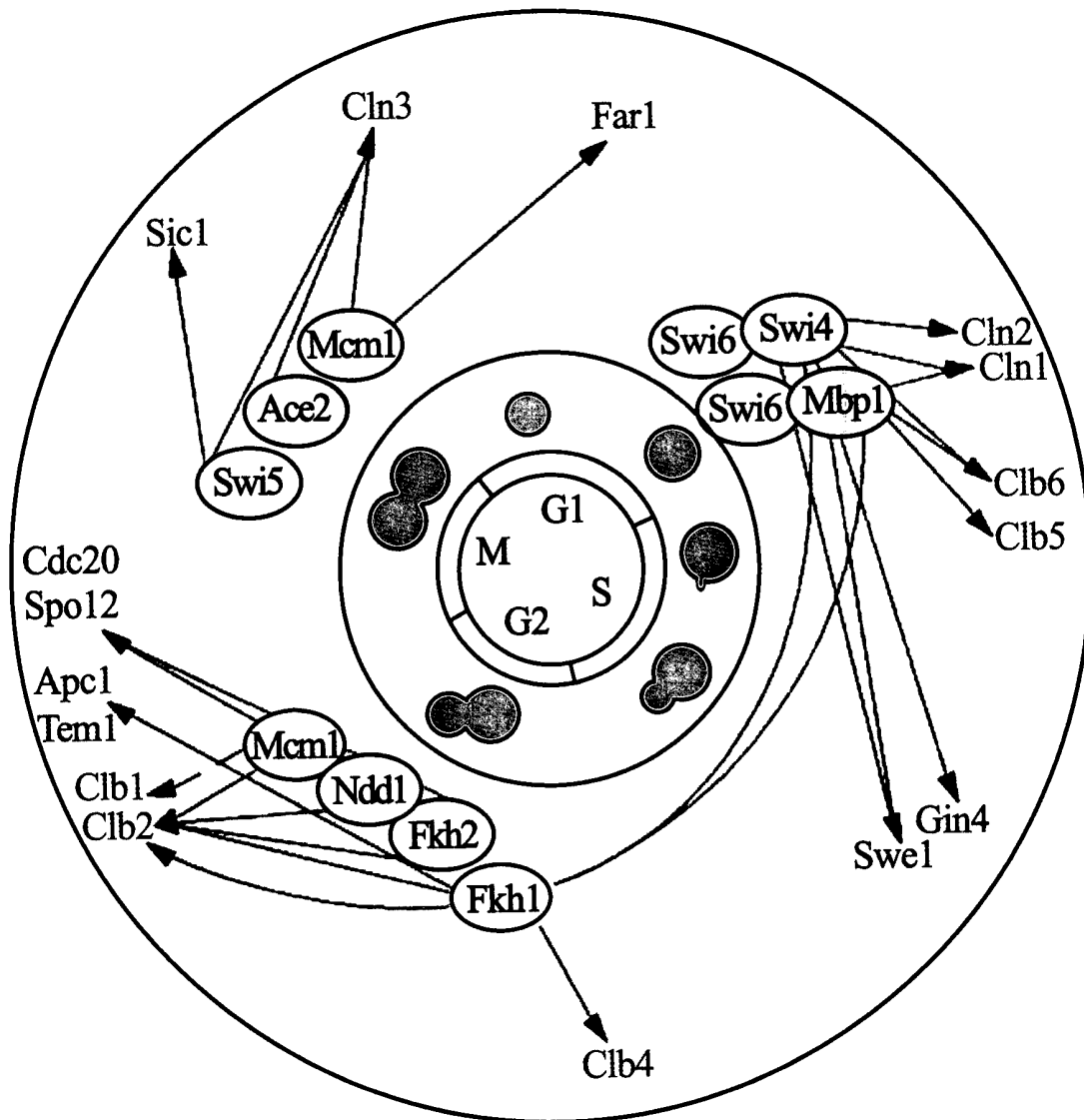


FIGURE 12B

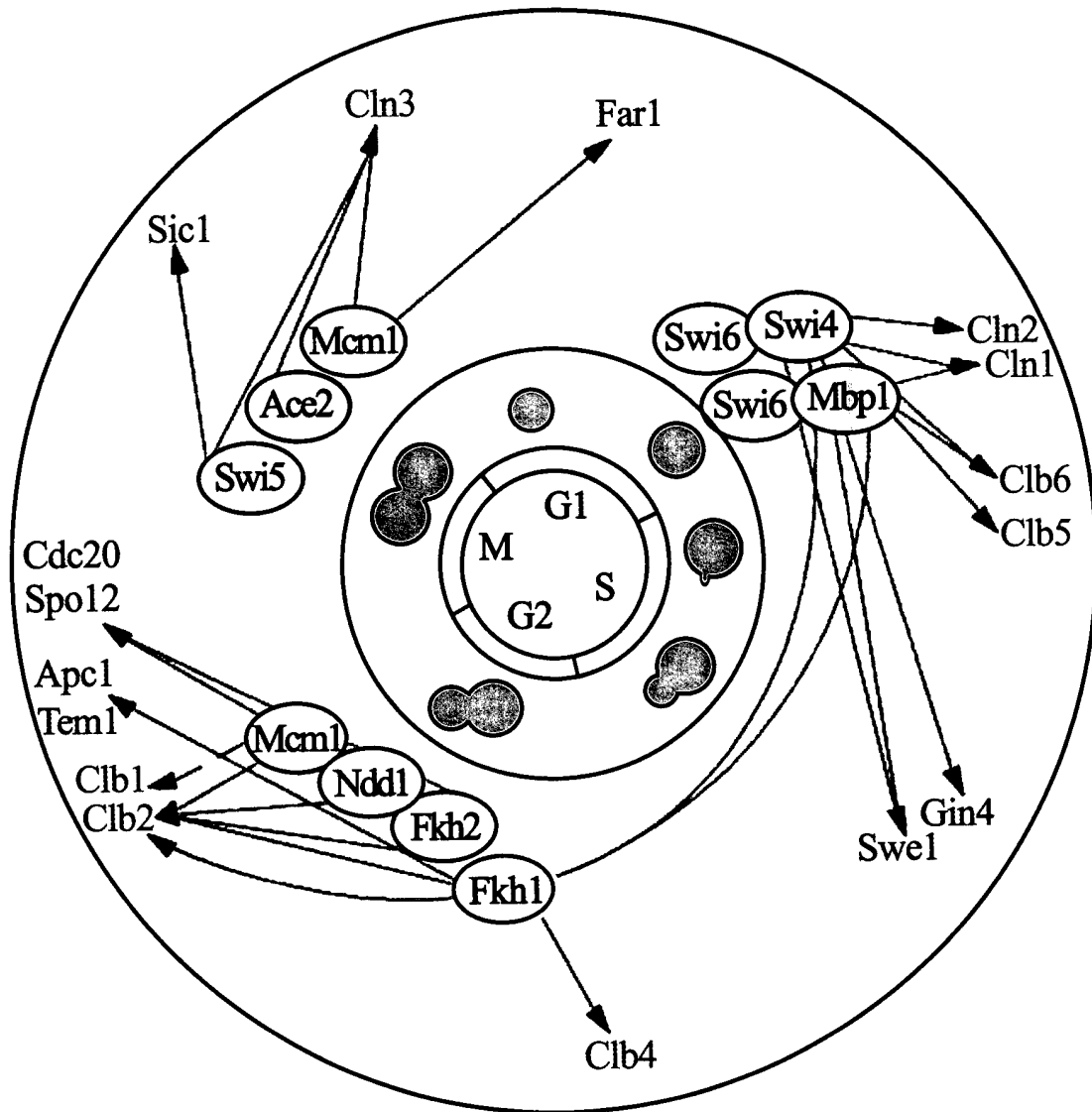


FIGURE 12B

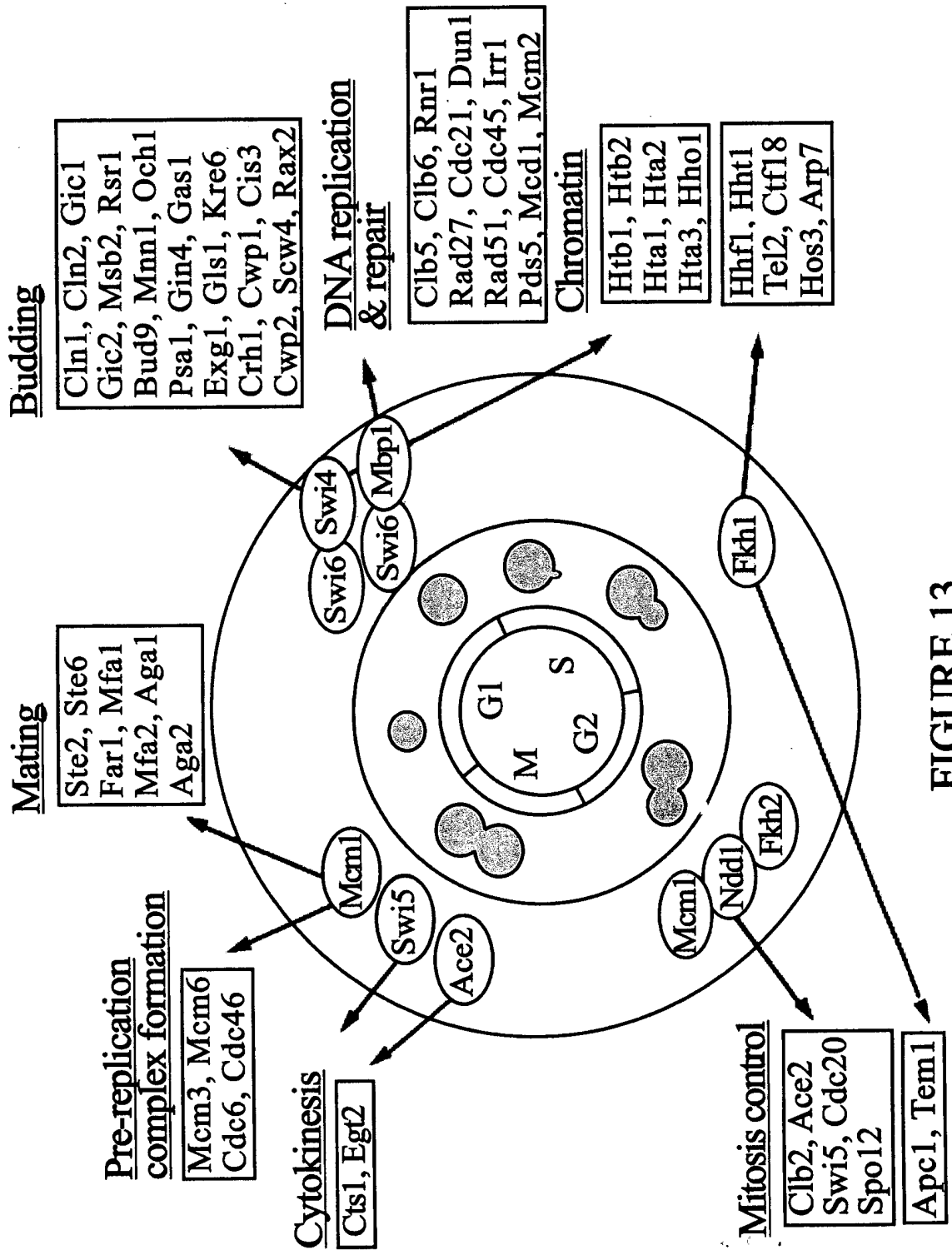
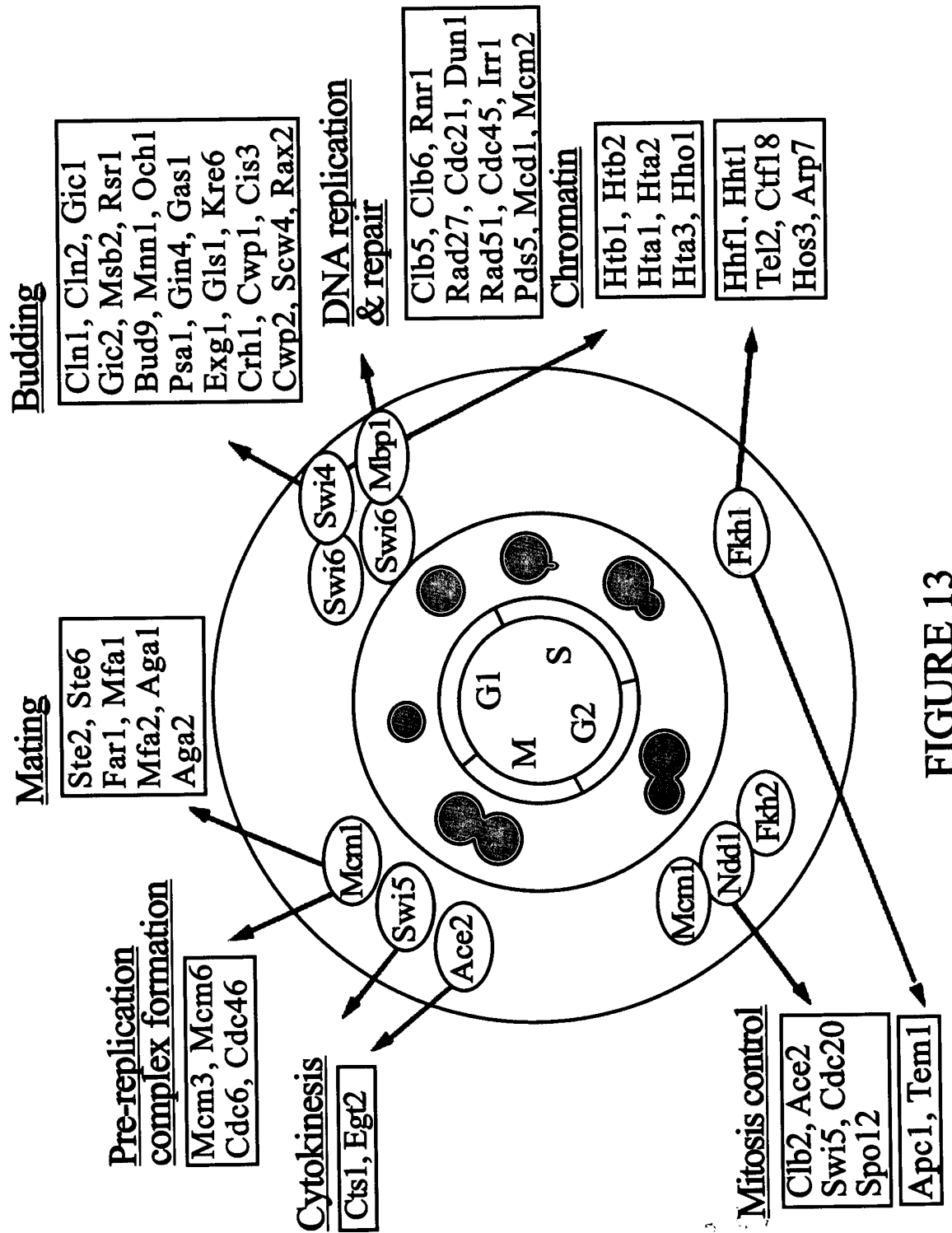


FIGURE 13



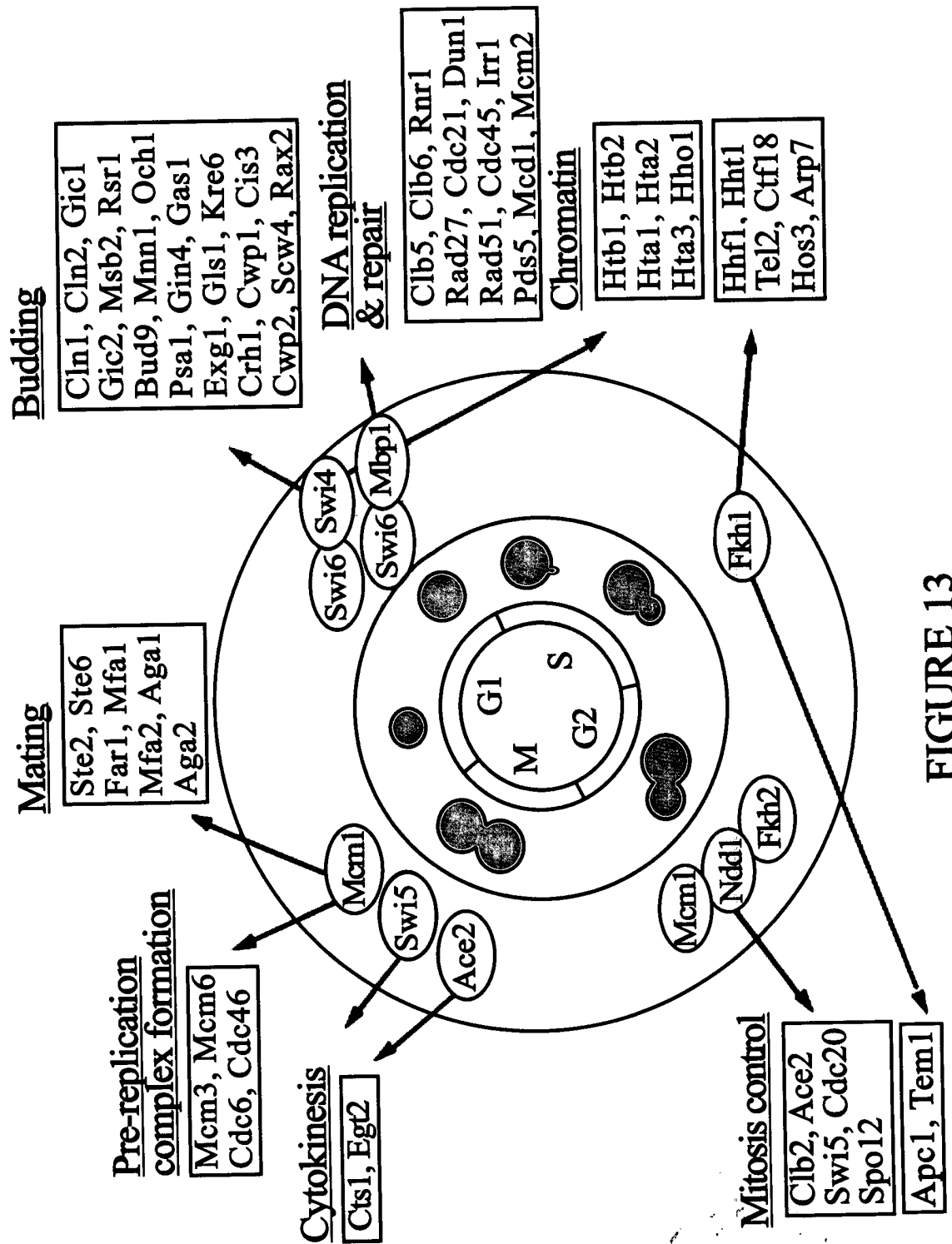


FIGURE 13

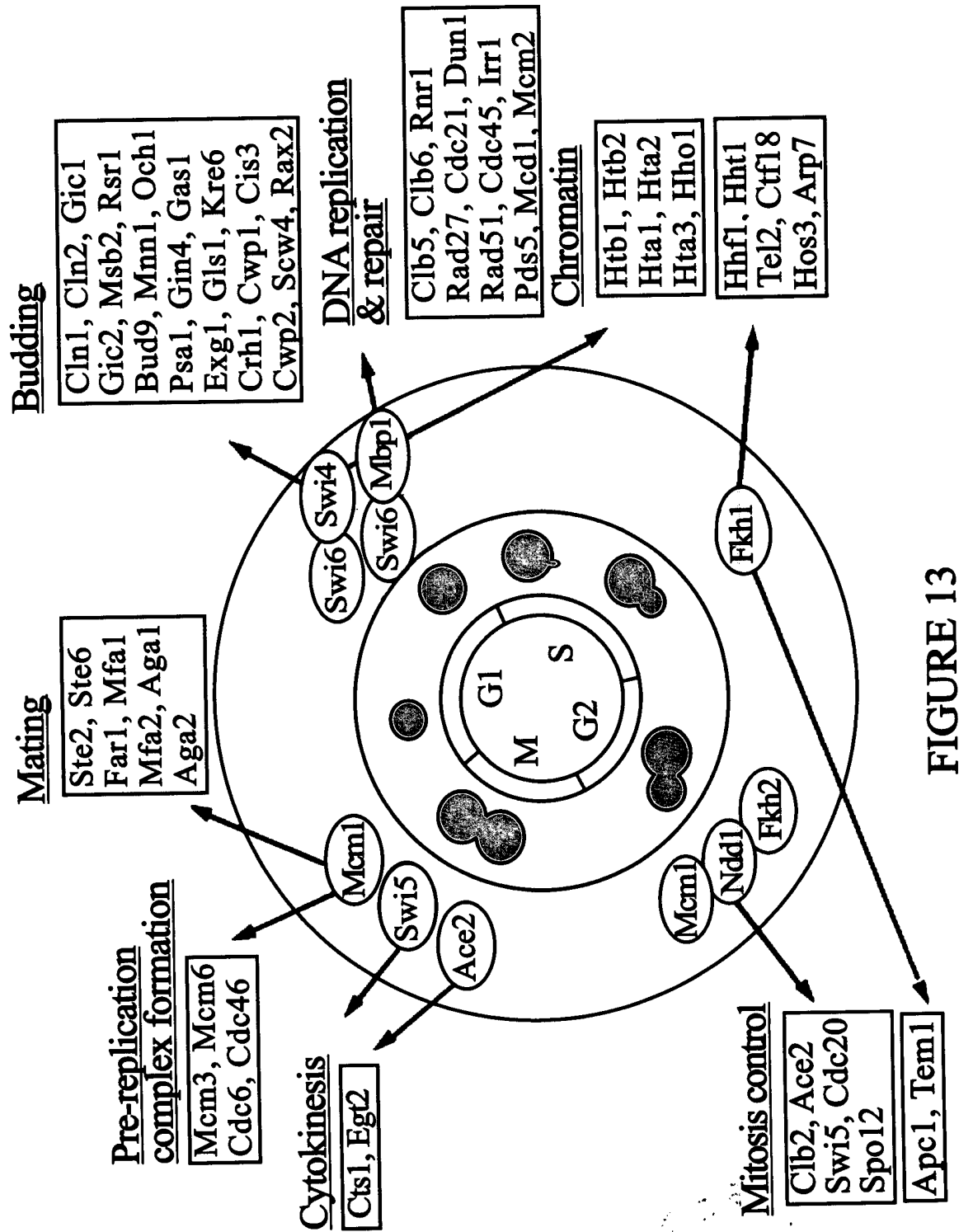


FIGURE 13

Figure 14A

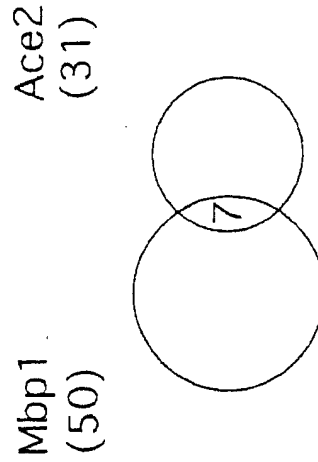
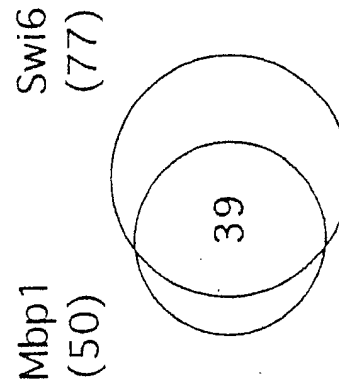
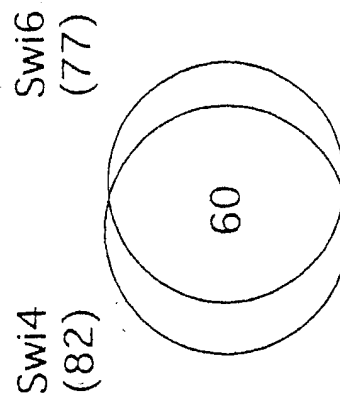
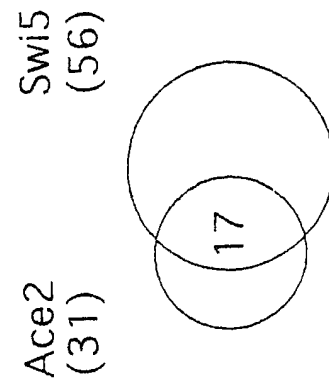
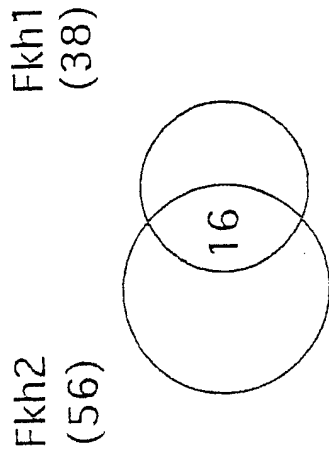
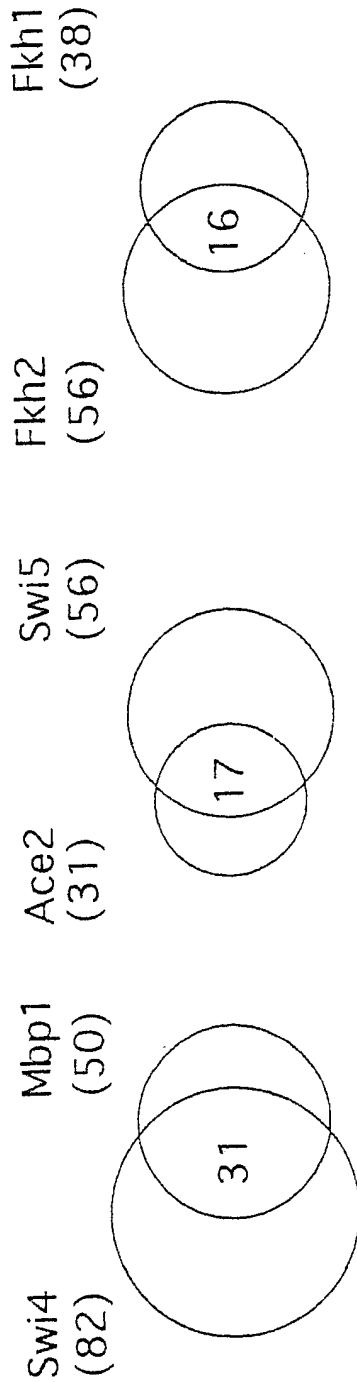


Figure 14B

Figure 14C